GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:14:54 ; Search time 2.63862 Seconds
(without alignments)
601.551 Million cell updates/sec

Title: US-09-869-414A-64
Perfect score: 49
Sequence: 1 SEVKMDAEFR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	100.0	10	13	AAR24261	Human amyloidin pr
2	49	100.0	10	21	AAY69703	Beta-APP alpha-sec
3	49	100.0	10	22	AAE10654	Human wild-type AP
4	49	100.0	10	22	AAE06899	Human amyloid prec
5	49	100.0	10	22	AAU06628	Asp2 recognition s
6	49	100.0	10	22	AAU07227	Human beta-amyloid
7	49	100.0	10	22	AAE02606	Human wild-type AP
8	49	100.0	10	22	AAB66574	Synthetic peptide
9	49	100.0	10	22	AAB46208	Human APP derived
10	49	100.0	10	22	AAB61336	Sythetic peptide f
11	49	100.0	10	23	ABG78375	Human beta amyloid
12	49	100.0	10	23	ABG30940	Nogo/BACE method c
13	49	100.0	10	23	AAU99490	Peptide #1 used as
14	49	100.0	10	23	ABB78615	Beta-secretase spe
15	49	100.0	10	23	ABB06426	Human APP beta-sec
16	49	100.0	10	24	ABG76103	Amyloid precursor
17	49	100.0	11	22	AAB75143	APP beta-secretase
18	49	100.0	11	22	AAB75144	Asp 1 substrate se
19	49	100.0	11	22	AAB97468	Asp2 substrate wil
20	49	100.0	12	23	ABB08997	Amyloid precursor
21	49	100.0	12	23	ABB07592	Biotinylated synth
22	49	100.0	12	23	AAE16657	APP substrate pept
23	49	100.0	12	23	AAU74831	Synthetic amyloid
24	49	100.0	12	24	AAO26795	Beta-secretase sub
25	49	100.0	13	19	AAW70869	Beta-amyloid pepti
26	49	100.0	13	23	AAM50891	Fluorescent substr
27	49	100.0	13	24	ABP71624	Beta-secretase act
28	49	100.0	13	24	ABG75934	Synthetic Amyloid
29	49	100.0	13	24	ABP71462	Beta-secretase act
30	49	100.0	13	24	ABP71263	Synthetic APP subs
31	49	100.0	13	24	AAO16443	Beta-secretase syn
32	49	100.0	13	24	ABP57078	Synthetic amyloid
33	49	100.0	13	24	ABP58369	Synthetic amyloid
34	49	100.0	16	21	AAB06315	Human beta-amyloid
35	49	100.0	16	21	AAB06317	Human beta-amyloid
36	49	100.0	18	22	AAE00608	Beta-amyloid precu
37	49	100.0	20	21	AAY69713	Beta-APP alpha-sec
38	49	100.0	23	22	AAB75147	Asp 1 substrate se
39	49	100.0	23	22	AAB97473	Asp2 substrate wil
40	49	100.0	33	20	AAW98002	Amyloid precursor
41	49	100.0	39	21	AAY69717	Beta-APP alpha-sec
42	49	100.0	45	18	AAW26512	Amyloid precursor
43	49	100.0	45	18	AAW26392	Amyloid precursor
44	49	100.0	45	19	AAW44748	APP-REP 751 [BAP d
45	49	100.0	45	19	AAW42977	Deletion beta-amyl

ALIGNMENTS

```
RESULT 1
AAR24261
ID   AAR24261 standard; Protein; 10 AA.
XX
AC   AAR24261;
XX
DT   25-MAR-2003  (updated)
DT   09-NOV-1992  (first entry)
XX
DE   Human amyloidin protease substrate sequence #1.
XX
KW   Alzheimer's disease; beta amyloid precursor protein; APP; zinc;
KW   metalloprotease; hAP; protease inhibitor; APP592-601
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Acetylated-Ser"
XX
PN   WO9207068-A1.
XX
PD   30-APR-1992.
XX
PF   04-OCT-1991;   91WO-US07290.
XX
PR   05-OCT-1990;   90US-0594122.
PR   30-SEP-1991;   91US-0766351.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Dovey HF,  Johnstone EM,  Little SP,  McConlogue L,  Seubert PA;
PI   Sinha S;
XX
DR   WPI; 1992-167148/20.
XX
PT   Human amyloidin protease - used for cleaving Met-Asp bond in
PT   amyloid-like substrate for identifying protease inhibitors
XX
PS   Claim 1; Page 52; 62pp; English.
XX
CC   Claimed human amyloidin protease is defined by its ability to
CC   cleave the Met-Asp bond of this synthetic substrate. The substrate,
CC   which corresponds to residues 592 to 601 of the 695 amino acid APP,
CC   can be used in an assay for identifying inhibitors of proteases
CC   which cleave Met-Asp bonds, e.g. amyloidin, human skin chymase or
CC   rat mast cell protease I or II.
CC   See AAR24260-3, AAR24266-7 and AAQ24875-Q24887.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   10 AA;

  Query Match             100.0%;  Score 49;  DB 13;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00059;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10


RESULT 2
AAY69703
ID   AAY69703 standard; peptide; 10 AA.
XX
AC   AAY69703;
XX
DT   11-APR-2000  (first entry)
XX
DE   Beta-APP alpha-secretase substrate [KMD]-APP(-5,+5).
XX
KW   Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KW   cleavage site; beta-secretase; neurodegenerative disease;
KW   Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO9964587-A1.
XX
PD   16-DEC-1999.
XX
PF   04-JUN-1999;   99WO-FR01326.
XX
PR   05-JUN-1998;   98FR-0007068.
PR   31-MAR-1999;   99US-0122599.
XX
PA   (RHON ) RHONE-POULENC RORER SA.
PA   (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI   Rholam M,  Munoz-Gimenez N,  Moutaouakil M,  Cohen P,  Bertrand P;
XX
DR   WPI; 2000-097537/08.
XX
PT   Polypeptide with beta-secretase activity, specific for wild-type
PT   amyloid precursor protein, useful in treating  Alzheimer's disease  -
XX
PS   Example 3; Page 24; 44pp; French.
XX
CC   Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC   novel polypeptide with beta-secretase activity that can cleave
CC   specifically the natural beta-amyloid precursor protein (bAPP). Normal
CC   cleavage of the protein occurs between amino acids Met596-Asp597 and
CC   Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC   polypeptide is used to identify agents that interact specifically with
CC   it. These agents regulate metabolism of APP, particularly they slow down
CC   or reduce production of beta-amyloid, so can be used to treat
CC   neurodegenerative diseases, particularly Alzheimer's disease.
XX
SQ   Sequence   10 AA;

  Query Match             100.0%;  Score 49;  DB 21;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00059;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10


RESULT 3
AAE10654
ID   AAE10654 standard; peptide; 10 AA.
XX
AC   AAE10654;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human wild-type APP beta-secretase peptide, PHA-95812E.
XX
KW   Human; aspartyl protease 1; Asp1; amyloid precursor protein;
KW   Alzheimer's disease; AD; dementia;  neurofibrillary tangle; gliosis;
KW   amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW   APP beta-secretase peptide.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   5..6
XX
PN   GB2357767-A.
XX
PD   04-JUL-2001.
XX
PF   22-SEP-2000; 2000GB-0023315.
XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99US-0404133.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2001-444208/48.
XX
PT   Polypeptide comprising fragments of human aspartyl protease with
PT   amyloid precursor protein processing activity and alpha-secretase
PT   activity, for identifying modulators useful in treating Alzheimer's
PT   disease -
XX
PS   Example 12; Page 84; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC   Asp1 proteins which lack transmembrane domain or amino terminal
CC   domain or cytoplasmic domain and retains alpha-secretase activity
CC   and amyloid protein precursor (APP) processing activity. The proteins
CC   of the invention are useful for assaying hu-Asp1 alpha-secretase
CC   activity, which in turn is useful for identifying modulators of
```

CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is wild-type
CC human amyloid precursor protein (APP) beta-secretase specific
CC substrate peptide, PHA-95812E. This peptide is used for assaying
CC the beta-secretase activity of human Aspartyl protease 2a (Asp2a)
CC protein. The peptide is also used for determining the relationship
CC between Aspartyl protease 1 (Asp1) and APP protein.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
||||||||||
Db 1 SEVKMDAEFR 10

RESULT 4
AAE06899
ID AAE06899 standard; peptide; 10 AA.
XX
AC AAE06899;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human amyloid precursor protein wild-type beta-secretase peptide.
XX
KW Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein; APP;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW neuroprotective; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Cleavage-site 5..6
XX
PN WO200150829-A2.
XX
PD 19-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00799.
XX
PR 09-MAY-2001; 2001WO-IB00799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.

PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-483072/52.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
PS Claim 127; Page 80; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting
CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC blots. The present sequence is human amyloid precursor protein (APP)
CC wild type beta-secretase peptide used in beta-secretase assay.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
||||||||||
Db 1 SEVKMDAEFR 10

RESULT 5
AAU06628
ID AAU06628 standard; Peptide; 10 AA.
XX
AC AAU06628;
XX
DT 24-OCT-2001 (first entry)
XX
DE Asp2 recognition site from wild-type APP.
XX
KW Aspartyl protease; Asp2; beta-secretase; nootropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta.
XX
OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Cleavage-site 5

FT /label= Asp2_protease_cleavage_site

XX

PN WO200149098-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB00798.

XX

PR 09-MAY-2001; 2001WO-IB00798.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502549/55.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl

PT protease 2, lacking Asp2 transmembrane domain and retaining beta

PT secretase activity of Asp2 useful for identifying inhibitors of Asp2

PT activity -

XX

PS Claim 127; Page 101; 185pp; English.

XX

CC The invention relates to a purified polypeptide comprising a fragment of

CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2

CC transmembrane domain and the Asp2 protein, and where the polypeptide and

CC the fragment retain the beta-secretase activity of the mammalian Asp2

CC protein. The invention also details polynucleotides for the Asp

CC proteins and vectors expressing them, and a polypeptide (isoform of

CC amyloid protein precursor (APP)) comprising the amino acid sequence of an

CC APP or its fragment containing an APP cleavage site recognizable by a

CC mammalian beta-secretase, and further comprising two lysine residues at

CC the carboxyl terminus of the amino acid sequence of the mammalian APP or

CC APP fragment. Also included in the invention are methods of identifying

CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are

CC useful for treating Alzheimer's disease. APP is useful in methods for

CC identifying inhibitors or modulators of human Asp2 activity and

CC amyloid-beta (Abeta) peptide production. APP is also useful in designing

CC therapeutics for the treatment or prevention of Alzheimer's disease.

CC APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which

CC is associated with increased levels of Abeta processing is useful in

CC assays relating the Alzheimer's research. The expression vector is useful

CC for recombinantly expressing APP. Nucleic acids that hybridise to

CC Asp oligonucleotides are useful as probes or primers. The probes are

CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in

CC Northern and Southern blots. The present sequence is a peptide substrate

CC for Asp2 corresponding to the wild-type APP beta-secretase site.

XX

SQ Sequence 10 AA;

```
  Query Match             100.0%;  Score 49;  DB 22;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00059;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10


RESULT 6
AAU07227
ID   AAU07227 standard; Peptide; 10 AA.
XX
AC   AAU07227;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human beta-amyloid protein precursor, APP-beta40 and 42 secretase site.
XX
KW   Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW   aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW   beta-secretase; Alzheimer's disease; APP-beta40; APP-beta42.
XX
OS   Homo sapiens.
XX
PN   WO200149097-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00797.
XX
PR   09-MAY-2001; 2001WO-IB00797.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-502548/55.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity  -
XX
PS   Claim 127; Page 101; 185pp; English.
XX
CC   The invention relates to a novel purified polypeptide comprising a
CC   fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC   Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC   and the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. Also included is an isoform of amyloid protein precursor (APP)
CC   comprising the amino acid sequence of a APP or its fragment containing
CC   an APP cleavage site recognisable by a mammalian beta-secretase, and
```

CC   further comprising two lysine residues at the carboxyl terminus of the
CC   amino acid sequence of the mammalian APP or APP fragment. The
CC   polypeptides are used for assaying for modulators of beta-secretase
CC   activity; identifying agents that inhibit the APP processing activity
CC   of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC   modulate the activity of Asp2; and for reducing cellular production of
CC   amyloid beta (Abeta) from APP. Agents identified by the above methods
CC   are useful for treating Alzheimer's disease; and for identifying
CC   modulators of amyloid-beta (Abeta) peptide production, for use in
CC   designing therapeutics for the treatment or prevention of Alzheimer's
CC   disease. Probes and primers derived from Asp nucleic acid sequences
CC   are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC   Northern and Southern blots. The present sequence represents the
CC   amino acid sequence of human amyloid protein precursor, APP-beta40
CC   and APP-beta42 secretase sites.
XX
SQ   Sequence   10 AA;

  Query Match   100.0%; Score 49; DB 22; Length 10;
  Best Local Similarity   100.0%; Pred. No. 0.00059;
  Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SEVKMDAEFR 10
              ||||||||||
Db   1 SEVKMDAEFR 10

RESULT 7
AAE02606
ID   AAE02606 standard; peptide; 10 AA.
XX
AC   AAE02606;
XX
DT   10-AUG-2001 (first entry)
XX
DE   Human wild-type APP beta-secretase substrate peptide, PHA-95812E.
XX
KW   Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW   Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp2a;
KW   beta-secretase.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Cleavage-site   5..6
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US26080.
XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX

PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney M, Bienkowski MJ;
XX
DR WPI; 2001-290516/30.
XX
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease -
XX
PS Example 12; Page 85; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human wild-type amyloid
CC precursor protein (APP) beta-secretase specific substrate peptide,
CC PHA-95812E. This peptide is used for assaying the beta-secretase activity
CC of human Aspartyl protease 2a (Asp2a) protein. The peptide is also used
CC for determining the relationship between Aspartyl protease 1 (Asp1) and
CC APP protein.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10
```

RESULT 8
AAB66574
ID AAB66574 standard; Peptide; 10 AA.
XX
AC AAB66574;
XX
DT 12-APR-2001 (first entry)
XX
DE Synthetic peptide derived from APP beta-secretase site.
XX
KW Memapsin 2; nootropic; neuroprotective; amyloid precursor protein;
KW APP; memapsin 2 inhibitor; Alzheimer's disease.
XX
OS Synthetic.
XX
PN WO200100665-A2.
XX
PD 04-JAN-2001.
XX
PF 27-JUN-2000; 2000WO-US17742.
XX
PR 28-JUN-1999; 99US-0141363.
PR 30-NOV-1999; 99US-0168060.

PR 25-JAN-2000; 2000US-0177836.
PR 27-JAN-2000; 2000US-0178368.
PR 08-JUN-2000; 2000US-0210292.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA (UNII) UNIV ILLINOIS FOUND.
XX
PI Tang JJN, Hong L, Ghosh AK;
XX
DR WPI; 2001-137933/14.
XX
PT Novel memapsin 2 inhibitors which bind to active site of memapsin 2
PT having 2 catalytic aspartic residues and substrate binding cleft, used
PT to treat Alzheimer's disease by blocking amyloid precursor protein
PT cleavage -
XX
PS Disclosure; Page 11; 86pp; English.
XX
CC The present sequence is given in a specification relating to an inhibitor
CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
CC active site, which is defined by the presence of two catalytic aspartic
CC residues and a substrate binding cleft. The inhibitor is useful for
CC the treatment and diagnosis of Alzheimer's disease. It is useful in
CC screens for individuals with a genetic predisposition to Alzheimer's
CC disease. The inhibitor is useful as a reagent for specifically binding to
CC memapsin 2 or memapsin 2 analogues and for aiding in memapsin 2
CC isolation, purification and characterisation.
XX
SQ Sequence 10 AA;

  Query Match 100.0%; Score 49; DB 22; Length 10;
  Best Local Similarity 100.0%; Pred. No. 0.00059;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
    ||||||||||
Db 1 SEVKMDAEFR 10

RESULT 9
AAB46208
ID AAB46208 standard; peptide; 10 AA.
XX
AC AAB46208;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #4.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX

PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX
PS Disclosure; Figure 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
||||||||||
Db 1 SEVKMDAEFR 10

RESULT 10
AAB61336
ID AAB61336 standard; peptide; 10 AA.
XX
AC AAB61336;
XX
DT 02-APR-2001 (first entry)
XX
DE Sythetic peptide from beta amyloid precursor protein.
XX
KW Memapsin 2; catalyst; Alzheimer's.
XX
OS Unidentified.
XX

PN   WO200100663-A2.
XX
PD   04-JAN-2001.
XX
PF   27-JUN-2000; 2000WO-US17661.
XX
PR   28-JUN-1999;   99US-0141363.
PR   30-NOV-1999;   99US-0168060.
PR   25-JAN-2000; 2000US-0177836.
PR   27-JAN-2000; 2000US-0178368.
PR   08-JUN-2000; 2000US-0210292.
XX
PA   (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
PI   Tang JJN, Lin X, Koelsch G;
XX
DR   WPI; 2001-102885/11.
XX
PT   Purified recombinant catalytically active memapsin 2, used to screen
PT   inhibitors of it, which are used to treat and prevent Alzheimer's
PT   disease -
XX
PS   Claim 6; Page 11; 86pp; English.
XX
CC   The present invention relates to a purified recombinant
CC   catalytically active memapsin 2. The invention may be used for
CC   isolating inhibitors which are used to treat or prevent
CC   Alzheimer's disease. The invention may also be used to screen
CC   for individuals more genetically prone to develop Alzheimer's
CC   disease.
XX
SQ   Sequence   10 AA;

  Query Match   100.0%; Score 49; DB 22; Length 10;
  Best Local Similarity   100.0%; Pred. No. 0.00059;
  Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SEVKMDAEFR 10
              ||||||||||
Db   1 SEVKMDAEFR 10

RESULT 11
ABG78375
ID   ABG78375 standard; Peptide; 10 AA.
XX
AC   ABG78375;
XX
DT   15-NOV-2002 (first entry)
XX
DE   Human beta amyloid precursor protein beta secretase site #1.
XX
KW   Human; memapsin 2; aspartic protease; beta secretase;
KW   degenerative disease; Alzheimer's disease; amyloid precursor protein;
KW   APP; neuroprotective; nootropic; inhibitor; cleavage site;
KW   substrate side-chain preference.
XX

OS Homo sapiens.
XX
PN WO200253594-A2.
XX
PD 11-JUL-2002.
XX
PF 28-DEC-2001; 2001WO-US50826.
XX
PR 28-DEC-2000; 2000US-258705P.
PR 14-MAR-2001; 2001US-275756P.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA (UNII) UNIV ILLINOIS FOUND.
XX
PI Tang JJN, Koelsch G, Ghosh AK;
XX
DR WPI; 2002-619088/66.
XX
PT New memapsin 2 activity inhibitor useful in treatment of e.g.
PT Alzheimer's disease -
XX
PS Disclosure; Page 23; 74pp; English.
XX
CC The invention relates to an inhibitor of catalytically active memapsin 2
CC (an aspartic protease which can cleave at beta secretase sites), which
CC binds to the active site of memapsin 2 defined by the presence of two
CC catalytic aspartic residues and substrate binding cleft. Also
CC included is a method of determination of the substrate side-chain
CC preference in memapsin 2 sub-sites comprising: (a) reacting a mixture of
CC memapsin 2 substrates with memapsin 2, and determining the sub-site
CC preference of memapsin 2 by determining relative initial hydrolysis rates
CC of the mixture of memapsin 2 substrates; or (b) preparing a combinatorial
CC library of memapsin 2 inhibitors containing a base sequence taken from
CC OM99-2 (Glu-Val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of
CC inhibitors with memapsin 2 which binds to several inhibitors to generate
CC several bound memapsin 2, and detecting the bound memapsin 2 with an
CC antibody raised to memapsin 2 and an alkaline phosphatase conjugated
CC secondary antibody. The inhibitors may be used in the manufacture of a
CC medicament for the treatment of Alzheimer's disease since memapsin 2 may
CC be involved in the cleavage of amyloid precursor protein (APP), and for
CC determining the substrate side-chain preference in memapsin 2 sub-sites.
CC The present sequence represents a beta secretase cleavage site used
CC to determine the substrate specificity of human memapsin 2.
XX
SQ Sequence 10 AA;

  Query Match   100.0%; Score 49; DB 23; Length 10;
  Best Local Similarity   100.0%; Pred. No. 0.00059;
  Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SEVKMDAEFR 10
              ||||||||||
Db   1 SEVKMDAEFR 10

RESULT 12
ABG30940

ID ABG30940 standard; Peptide; 10 AA.
XX
AC ABG30940;
XX
DT 21-OCT-2002 (first entry)
XX
DE Nogo/BACE method cleavage peptide #1.
XX
KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
KW tissue hypertrophy; central nervous system; axon regeneration;
KW Nogo-associated disease; metastasis; cleavage peptide.
XX
OS Unidentified.
XX
FH Key   Location/Qualifiers
FT Cleavage-site   5..6
FT   /note= "Beta-secretase cleavage site"
XX
PN WO200257483-A2.
XX
PD 25-JUL-2002.
XX
PF 18-JAN-2002; 2002WO-GB00228.
XX
PR 18-JAN-2001; 2001GB-0001312.
XX
PA (GLAX) GLAXO GROUP LTD.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Blackstock WP, Hale RS, Prinjha R, Rowley A;
XX
DR WPI; 2002-599722/64.
XX
PT Identifying modulators of Nogo or BACE activity for treating acute
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
PT providing and monitoring interaction between Nogo and BACE polypeptides
PT -
XX
PS Disclosure; Page 14; 68pp; English.
XX
CC The present invention relates to a new method of identifying modulators
CC of Nogo function or BACE activity. The method involves providing Nogo and
CC BACE polypeptides capable of binding with each other, monitoring the
CC interaction between these polypeptides, and determining if the test agent
CC is a modulator of Nogo or BACE activity. The method is useful in treating
CC acute neuronal injuries, such as spinal or head injury, stroke,
CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,
CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.
CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue
CC hypertrophy) of the central nervous system. The BACE polypeptide is
CC useful in screening methods to identify agents that may act as modulators
CC of BACE activity and in particular agents that may be useful in treating
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
CC and the polynucleotide encoding the BACE polypeptide are useful in

CC manufacturing a medicament for the treatment or prevention of disorders
CC responsive to the modulation of Nogo activity, in alleviating the
CC symptoms or improving the condition of a patient suffering from this
CC disorder, in axon regeneration, or in preventing metastasis or spreading
CC of a cancer. The polynucleotide may also be an essential component in
CC assays, a probe, in recombinant protein synthesis, and in gene therapy
CC techniques. The present amino acid sequence represents a cleavage peptide
CC that was used in the methods of the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
||||||||||
Db 1 SEVKMDAEFR 10

RESULT 13
AAU99490
ID AAU99490 standard; peptide; 10 AA.
XX
AC AAU99490;
XX
DT 07-OCT-2002 (first entry)
XX
DE Peptide #1 used as substrate for human memapsin 2.
XX
KW Human; memapsin 2; beta secretase; aspartic protease; APP;
KW beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;
KW neuroprotective; nootropic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2002049303-A1.
XX
PD 25-APR-2002.
XX
PF 28-FEB-2001; 2001US-0796264.
XX
PR 28-JUN-1999; 99US-141363P.
PR 30-NOV-1999; 99US-168060P.
PR 25-JAN-2000; 2000US-177836P.
PR 27-JAN-2000; 2000US-178368P.
PR 27-JUN-2000; 2000US-0604608.
XX
PA (TANG/) TANG J J N.
PA (LINX/) LIN X.
PA (KOEL/) KOELSCH G.
PA (HONG/) HONG L.
XX
PI Tang JJN, Lin X, Koelsch G, Hong L;
XX
DR WPI; 2002-507280/54.

XX
PT New recombinant catalytically active memapsin 2, useful to screen for
PT inhibitors of memapsin 2 which can be used to prevent and treat
PT Alzheimer's disease -
XX
PS Claim 6; Page 30; 44pp; English.
XX
CC The present invention relates to methods for the production of
CC purified, recombinant catalytically active, memapsin 2 (beta
CC secretase). Memapsin 2, a member of the aspartic protease family,
CC cleaves beta-amyloid precursor protein (APP) found in amyloid plaques.
CC The recombinant memapsin 2 is useful for identifying inhibitors of
CC memapsin 2 in the design of drugs for the treatment and/or prevention
CC of Alzheimer's disease. The recombinant memapsin 2 can be used to
CC immunise against Alzheimer's disease. The present sequence represents
CC a peptide used as a substrate for human memapsin 2.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
||||||||||
Db 1 SEVKMDAEFR 10

RESULT 14
ABB78615
ID ABB78615 standard; Peptide; 10 AA.
XX
AC ABB78615;
XX
DT 16-JUL-2002 (first entry)
XX
DE Beta-secretase specific substrate PHA-95812E SEQ ID NO:64.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW proteolytic.
XX
OS Synthetic.
XX
PN GB2367060-A.
XX
PD 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-0025934.
XX
PR 23-SEP-1999; 99US-155493P.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-169232P.
PR 22-SEP-2000; 2000GB-0023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.

XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2002-396337/43.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect
PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT disease -
XX
PS Example 15; Page 92; 182pp; English.
XX
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the
CC non-coding strand complementary to a defined 1804 nucleotide sequence
CC (see ABL52456) where the nucleotide sequence encodes a polypeptide having
CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents a beta-secretase specific substrate peptide which is
CC used in an example from the present invention.
XX
SQ Sequence 10 AA;

  Query Match   100.0%; Score 49; DB 23; Length 10;
  Best Local Similarity   100.0%; Pred. No. 0.00059;
  Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SEVKMDAEFR 10
              ||||||||||
Db   1 SEVKMDAEFR 10

RESULT 15
ABB06426
ID ABB06426 standard; Peptide; 10 AA.
XX
AC ABB06426;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human APP beta-secretase cleavage sequence SEQ ID NO:20.
XX

KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200206306-A2.
XX
PD 24-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US23035.
XX
PR 19-JUL-2000; 2000US-219795P.
PR 12-MAR-2001; 2001US-275251P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
PI Heinrikson RL;
XX
DR WPI; 2002-216995/27.
XX
PT Novel substrates for human aspartyl protease useful for identifying
PT modulators of beta secretase activity of aspartyl protease for treating
PT Alzheimer's disease -
XX
PS Claim 18; Page 126; 188pp; English.
XX
CC The present invention describes an isolated peptide (I) comprising a
CC sequence of at least four amino acids, where the peptide is a substrate
CC for conducting aspartyl protease assays. (I) has neuroprotective and
CC nootropic activities, and can be used as an inhibitor of beta-secretase
CC activity. A beta-secretase modulator from the present invention can be
CC used for inhibiting beta-secretase activity in vivo, and in the
CC manufacture of a medicament for the treatment of Alzheimer's disease.
CC Pharmaceutical compositions from the present invention can be used for
CC treating a disease or condition characterised by an abnormal beta-
CC secretase activity. (I) is useful for identifying agents that modulate
CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
CC as a core structure to construct derivatives. ABL49914 to ABL49925 and
CC ABB06409 to ABB06593 represent sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SEVKMDAEFR 10
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Db          1 SEVKMDAEFR 10
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Job time : 3.63862 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:19:55 ; Search time 0.898662 Seconds
(without alignments)
470.821 Million cell updates/sec

Title: US-09-869-414A-64
Perfect score: 49
Sequence: 1 SEVKMDAEFR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	100.0	10	4	US-09-548-372D-64	Sequence 64, Appl
2	49	100.0	10	4	US-09-548-367D-64	Sequence 64, Appl
3	49	100.0	10	4	US-09-551-853D-64	Sequence 64, Appl
4	49	100.0	10	4	US-09-604-608-4	Sequence 4, Appli
5	49	100.0	11	5	PCT-US94-07043A-7	Sequence 7, Appli
6	49	100.0	12	5	PCT-US94-07043A-2	Sequence 2, Appli
7	49	100.0	16	5	PCT-US94-07043A-1	Sequence 1, Appli
8	49	100.0	27	1	US-08-141-324-11	Sequence 11, Appl
9	49	100.0	27	1	US-08-541-902-11	Sequence 11, Appl
10	49	100.0	45	1	US-08-462-859A-5	Sequence 5, Appli
11	49	100.0	45	1	US-08-123-659A-5	Sequence 5, Appli

12	49	100.0	45	1	US-08-464-247A-5	Sequence 5, Appli
13	49	100.0	45	1	US-08-464-248A-5	Sequence 5, Appli
14	49	100.0	58	1	US-08-371-930-25	Sequence 25, Appl
15	49	100.0	58	5	PCT-US94-01712-25	Sequence 25, Appl
16	49	100.0	63	1	US-08-462-859A-3	Sequence 3, Appli
17	49	100.0	63	1	US-08-462-859A-4	Sequence 4, Appli
18	49	100.0	63	1	US-08-123-659A-3	Sequence 3, Appli
19	49	100.0	63	1	US-08-123-659A-4	Sequence 4, Appli
20	49	100.0	63	1	US-08-464-247A-3	Sequence 3, Appli
21	49	100.0	63	1	US-08-464-247A-4	Sequence 4, Appli
22	49	100.0	63	1	US-08-464-248A-3	Sequence 3, Appli
23	49	100.0	63	1	US-08-464-248A-4	Sequence 4, Appli
24	49	100.0	105	2	US-08-729-345-1	Sequence 1, Appli
25	49	100.0	117	2	US-08-729-345-3	Sequence 3, Appli
26	49	100.0	152	6	5187153-4	Patent No. 5187153
27	49	100.0	162	6	5220013-4	Patent No. 5220013
28	49	100.0	162	6	5223482-4	Patent No. 5223482
29	49	100.0	264	1	US-07-990-893-5	Sequence 5, Appli
30	49	100.0	487	1	US-08-462-859A-9	Sequence 9, Appli
31	49	100.0	487	1	US-08-123-659A-9	Sequence 9, Appli
32	49	100.0	487	1	US-08-464-247A-9	Sequence 9, Appli
33	49	100.0	487	1	US-08-464-248A-9	Sequence 9, Appli
34	49	100.0	492	1	US-08-462-859A-7	Sequence 7, Appli
35	49	100.0	492	1	US-08-123-659A-7	Sequence 7, Appli
36	49	100.0	492	1	US-08-464-247A-7	Sequence 7, Appli
37	49	100.0	492	1	US-08-464-248A-7	Sequence 7, Appli
38	49	100.0	537	1	US-08-453-552-4	Sequence 4, Appli
39	49	100.0	537	2	US-08-710-637-4	Sequence 4, Appli
40	49	100.0	537	5	PCT-US93-00907-4	Sequence 4, Appli
41	49	100.0	656	1	US-08-371-930-23	Sequence 23, Appl
42	49	100.0	656	5	PCT-US94-01712-23	Sequence 23, Appl
43	49	100.0	676	1	US-08-371-930-24	Sequence 24, Appl
44	49	100.0	676	5	PCT-US94-01712-24	Sequence 24, Appl
45	49	100.0	694	1	US-08-339-152A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-548-372D-64
; Sequence 64, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-372D-64

Query Match 100.0%; Score 49; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
||||||||||
Db 1 SEVKMDAEFR 10

RESULT 2
US-09-548-367D-64
; Sequence 64, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-367D-64

Query Match 100.0%; Score 49; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
||||||||||

```
Db          1 SEVKMDAEFR 10


RESULT 3
US-09-551-853D-64
; Sequence 64, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-09-551-853D-64

  Query Match             100.0%;  Score 49;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00061;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10


RESULT 4
US-09-604-608-4
; Sequence 4, Application US/09604608
; Patent No. 6545127
; GENERAL INFORMATION:
;  APPLICANT:  Tang, Jordan J.N.
;  APPLICANT:  Lin, Xinli
;  APPLICANT:  Koelsch, Gerald
;  TITLE OF INVENTION:  Catalytically Active Recombinant Memapsin and Methods
;  TITLE OF INVENTION:  of Use Thereof
;  FILE REFERENCE:  OMRF 179
;  CURRENT APPLICATION NUMBER: US/09/604,608
;  CURRENT FILING DATE:  2000-06-27
;  PRIOR APPLICATION NUMBER:  60/141,363
;  PRIOR FILING DATE:  1999-06-28
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;  PRIOR APPLICATION NUMBER:  60/168,060
;  PRIOR FILING DATE:  1999-11-30
;  PRIOR APPLICATION NUMBER:  60/177,836
;  PRIOR FILING DATE:  2000-01-25
;  PRIOR APPLICATION NUMBER:  60/178,368
;  PRIOR FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  60/210,292
;  PRIOR FILING DATE:  2000-06-08
;  NUMBER OF SEQ ID NOS:  31
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-604-608-4

  Query Match             100.0%;  Score 49;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.00061;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10


RESULT 5
PCT-US94-07043A-7
; Sequence 7, Application PC/TUS9407043A
;  GENERAL INFORMATION:
;    APPLICANT:  Tamburini, Paul P.; Benz, G nter; H bich,
;    APPLICANT:  Dieter; Dreyer, Robert N.; Koenig, Gerhard
;    TITLE OF INVENTION:  CATHEPSIN D IS AN AMYLOIDOGENIC
;    TITLE OF INVENTION:  PROTEASE IN ALZHEIMER S DISEASE
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miles Inc.
;      STREET:  400 Morgan Lane
;      CITY:  West Haven
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06516
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 800 kb storage
;      COMPUTER:  Sharp PC 4600
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/07043A
;      FILING DATE:  June 21, 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/10889
;      FILING DATE:  November 12, 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/995,660
```

```
;       FILING DATE:  December 16, 1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/880,914
;       FILING DATE:  May 11, 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Pamela A. Simonton
;       REGISTRATION NUMBER:  31,060
;       REFERENCE/DOCKET NUMBER:  MTI 224.3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (203) 937-2340
;       TELEFAX:  (203) 937-2795
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
PCT-US94-07043A-7

  Query Match             100.0%;  Score 49;  DB 5;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.00067;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          2 SEVKMDAEFR 11


RESULT 6
PCT-US94-07043A-2
; Sequence 2, Application PC/TUS9407043A
;  GENERAL INFORMATION:
;    APPLICANT:  Tamburini, Paul P.; Benz, G nter; H bich,
;    APPLICANT:  Dieter; Dreyer, Robert N.; Koenig, Gerhard
;    TITLE OF INVENTION:  CATHEPSIN D IS AN AMYLOIDOGENIC
;    TITLE OF INVENTION:  PROTEASE IN ALZHEIMER S DISEASE
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miles Inc.
;      STREET:  400 Morgan Lane
;      CITY:  West Haven
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06516
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 800 kb storage
;      COMPUTER:  Sharp PC 4600
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/07043A
;      FILING DATE:  June 21, 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/10889
;      FILING DATE:  November 12, 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/995,660
```

```
;       FILING DATE:  December 16, 1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/880,914
;       FILING DATE:  May 11, 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Pamela A. Simonton
;       REGISTRATION NUMBER:  31,060
;       REFERENCE/DOCKET NUMBER:  MTI 224.3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (203) 937-2340
;       TELEFAX:  (203) 937-2795
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  12 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
PCT-US94-07043A-2

  Query Match             100.0%;  Score 49;  DB 5;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.00073;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          2 SEVKMDAEFR 11


RESULT 7
PCT-US94-07043A-1
; Sequence 1, Application PC/TUS9407043A
;  GENERAL INFORMATION:
;    APPLICANT:  Tamburini, Paul P.; Benz, G nter; H bich,
;    APPLICANT:  Dieter; Dreyer, Robert N.; Koenig, Gerhard
;    TITLE OF INVENTION:  CATHEPSIN D IS AN AMYLOIDOGENIC
;    TITLE OF INVENTION:  PROTEASE IN ALZHEIMER S DISEASE
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miles Inc.
;      STREET:  400 Morgan Lane
;      CITY:  West Haven
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06516
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 800 kb storage
;      COMPUTER:  Sharp PC 4600
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/07043A
;      FILING DATE:  June 21, 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/10889
;      FILING DATE:  November 12, 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/995,660
```

```
;       FILING DATE:  December 16, 1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/880,914
;       FILING DATE:  May 11, 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Pamela A. Simonton
;       REGISTRATION NUMBER:  31,060
;       REFERENCE/DOCKET NUMBER:  MTI 224.3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (203) 937-2340
;       TELEFAX:  (203) 937-2795
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
PCT-US94-07043A-1

  Query Match             100.0%;  Score 49;  DB 5;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 0.001;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          2 SEVKMDAEFR 11


RESULT 8
US-08-141-324-11
; Sequence 11, Application US/08141324
; Patent No. 5475097
;  GENERAL INFORMATION:
;    APPLICANT:  Travis, James
;    APPLICANT:  Potempa, Jan S.
;    APPLICANT:  Barr, Philip J.
;    APPLICANT:  Pavloff, Nadine
;    APPLICANT:  Pike, Robert N.
;    TITLE OF INVENTION:  Lysine-specific Porphyromonas gingivalis
;    TITLE OF INVENTION:  Protease
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Greenlee and Winner, P.C.
;      STREET:  5370 Manhattan Circle, Suite 201
;      CITY:  Boulder
;      STATE:  CO
;      COUNTRY:  US
;      ZIP:  80303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/141,324
;      FILING DATE:  21-OCT-1993
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  Ferber, Donna M.
;       REGISTRATION NUMBER:  33,878
;       REFERENCE/DOCKET NUMBER:  44-93
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  303-499-8080
;       TELEFAX:  303-499-8089
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  27 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
US-08-141-324-11

  Query Match             100.0%;  Score 49;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          4 SEVKMDAEFR 13


RESULT 9
US-08-541-902-11
; Sequence 11, Application US/08541902
; Patent No. 5707620
;  GENERAL INFORMATION:
;     APPLICANT:  Travis, James
;     APPLICANT:  Potempa, Jan S.
;     APPLICANT:  Barr, Philip J.
;     APPLICANT:  Pavloff, Nadine
;     APPLICANT:  Pike, Robert N.
;     TITLE OF INVENTION:  Lysine-specific Porphyromonas gingivalis
;     TITLE OF INVENTION:  Protease
;     NUMBER OF SEQUENCES:  28
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Greenlee and Winner, P.C.
;       STREET:  5370 Manhattan Circle, Suite 201
;       CITY:  Boulder
;       STATE:  CO
;       COUNTRY:  US
;       ZIP:  80303
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/541,902
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/141,324
```

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;       FILING DATE:  21-OCT-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ferber, Donna M.
;       REGISTRATION NUMBER:  33,878
;       REFERENCE/DOCKET NUMBER:  44-93
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  303-499-8080
;       TELEFAX:  303-499-8089
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  27 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
US-08-541-902-11

  Query Match             100.0%;  Score 49;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          4 SEVKMDAEFR 13


RESULT 10
US-08-462-859A-5
; Sequence 5, Application US/08462859A
; Patent No. 5652092
;  GENERAL INFORMATION:
;     APPLICANT:  Jacobsen, J. S.
;     APPLICANT:  Vitek, M. P.
;     TITLE OF INVENTION:  No. 5652092el Amyloid Precursor and Method of
;     TITLE OF INVENTION:  Using Same to Access Agents Which Down-Regulate
Formation
;     TITLE OF INVENTION:  of B-Amyloid Peptide
;     NUMBER OF SEQUENCES:  19
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  American Cyanamid Company
;       STREET:  One Cyanamid Plaza
;       CITY:  Wayne
;       STATE:  New Jersey
;       COUNTRY:  United States
;       ZIP:  07470-8426
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/462,859A
;       FILING DATE:  05-JUN-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  Barnhard, Elizabeth M.
;       REGISTRATION NUMBER:  31,088
;       REFERENCE/DOCKET NUMBER:  31,844-04
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (201)831-3246
;       TELEFAX:  (201)831-3305
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  45 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-462-859A-5

  Query Match             100.0%;  Score 49;  DB 1;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.003;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          5 SEVKMDAEFR 14


RESULT 11
US-08-123-659A-5
; Sequence 5, Application US/08123659A
; Patent No. 5656477
;  GENERAL INFORMATION:
;     APPLICANT:  Jacobsen, J. S.
;     APPLICANT:  Vitek, M. P.
;     TITLE OF INVENTION:  No. 5656477el Amyloid Precursor and Method of
;     TITLE OF INVENTION:  Using Same to Access Agents Which Down-Regulate
Formation
;     TITLE OF INVENTION:  of B-Amyloid Peptide
;     NUMBER OF SEQUENCES:  19
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Anne Rosenblum
;       STREET:  163 Delaware Avenue, Suite 212
;       CITY:  Delmar
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  12054
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/123,659A
;       FILING DATE:  20-SEP-1993
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Rosenblum, Anne M.
;       REGISTRATION NUMBER:  30,419
;       REFERENCE/DOCKET NUMBER:  31,844-01
;     TELECOMMUNICATION INFORMATION:
```

```
;       TELEPHONE:  (518)475-0611
;       TELEFAX:  (518)475-0619
;  INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  45 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-123-659A-5

  Query Match             100.0%;  Score 49;  DB 1;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.003;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          5 SEVKMDAEFR 14


RESULT 12
US-08-464-247A-5
; Sequence 5, Application US/08464247A
; Patent No. 5693478
;  GENERAL INFORMATION:
;     APPLICANT:  Jacobsen, J. S.
;     APPLICANT:  Vitek, M. P.
;     TITLE OF INVENTION:  No. 5693478el Amyloid Precursor and Method of
;     TITLE OF INVENTION:  Using Same to Access Agents Which Down-Regulate
Formation
;     TITLE OF INVENTION:  of B-Amyloid Peptide
;     NUMBER OF SEQUENCES:  19
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  American Cyanamid Company
;       STREET:  One Campus Drive
;       CITY:  Parsippany
;       STATE:  New Jersey
;       COUNTRY:  United States
;       ZIP:  07054
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/464,247A
;       FILING DATE:  05-JUN-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Barnhard, Elizabeth M.
;       REGISTRATION NUMBER:  31,088
;       REFERENCE/DOCKET NUMBER:  31,844-03
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-683-2158
;       TELEFAX:  201-683-4117
;  INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  45 amino acids
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:16:55 ; Search time 0.917782 Seconds
(without alignments)
1047.838 Million cell updates/sec

Title: US-09-869-414A-64
Perfect score: 49
Sequence: 1 SEVKMDAEFR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	100.0	57	2	E60045	Alzheimer's diseas
2	49	100.0	57	2	F60045	Alzheimer's diseas
3	49	100.0	57	2	G60045	Alzheimer's diseas
4	49	100.0	57	2	D60045	Alzheimer's diseas
5	49	100.0	57	2	A60045	Alzheimer's diseas
6	49	100.0	57	2	B60045	Alzheimer's diseas
7	49	100.0	82	2	PQ0438	Alzheimer's diseas
8	49	100.0	695	1	A49795	Alzheimer's diseas
9	49	100.0	770	1	QRHUA4	Alzheimer's diseas
10	44	89.8	33	2	S23094	beta-amyloid prote
11	44	89.8	695	2	A27485	Alzheimer's diseas
12	44	89.8	695	2	S00550	Alzheimer's diseas
13	43	87.8	747	2	JH0773	Alzheimer's diseas

14	39	79.6	142	2	E89026	protein F13A2.1 [i
15	35	71.4	774	2	AG1565	autolysin (amidase
16	34	69.4	626	2	AF0358	conserved hypothet
17	34	69.4	3562	2	A47171	chondroitin sulfat
18	34	69.4	4563	1	LPHUB	apolipoprotein B-1
19	33	67.3	927	2	T38127	phosphoprotein - f
20	33	67.3	1245	2	G86404	probable P-glycopr
21	32	65.3	263	2	D84226	hypothetical prote
22	32	65.3	354	2	S51143	FMO-protein - Chlo
23	32	65.3	392	2	T49471	mucin (muc3) relat
24	32	65.3	426	2	G75187	probable trehalose
25	32	65.3	625	2	D86244	protein Ser/Thr pr
26	32	65.3	700	2	E84131	transcription anti
27	32	65.3	929	2	T52517	hypothetical prote
28	32	65.3	1044	2	H97186	glycosyltransferas
29	32	65.3	1265	2	T51498	hypothetical prote
30	32	65.3	1906	2	AD2443	hypothetical prote
31	32	65.3	2514	2	T37320	ataxia telangiecta
32	32	65.3	2619	2	T24588	hypothetical prote
33	31	63.3	87	2	A97842	hypothetical prote
34	31	63.3	155	2	F75040	hypothetical prote
35	31	63.3	178	2	C64168	hypothetical prote
36	31	63.3	182	2	AC0449	conserved hypothet
37	31	63.3	183	2	S56460	probable alpha hel
38	31	63.3	183	2	AD1056	conserved hypothet
39	31	63.3	183	2	C86121	probable alpha hel
40	31	63.3	183	2	C91280	probable alpha hel
41	31	63.3	198	2	S48290	OX40 ligand - mous
42	31	63.3	199	2	F72060	conserved hypothet
43	31	63.3	199	2	C86564	CT471 hypothetical
44	31	63.3	226	2	G69129	hypothetical prote
45	31	63.3	279	2	T41124	single-stranded DN

ALIGNMENTS

RESULT 1
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: E60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: E60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56130
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

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  Query Match             100.0%;  Score 49;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.0018;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10
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```
RESULT 2
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: F60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
```

```
  Query Match             100.0%;  Score 49;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.0018;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10
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```
RESULT 3
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: G60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: G60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56126
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
```

```
  Query Match             100.0%;  Score 49;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.0018;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10
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RESULT 4
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: D60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: D60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

```
  Query Match             100.0%;  Score 49;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.0018;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10
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RESULT 5
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: A60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56125
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match 100.0%; Score 49; DB 2; Length 57;
  Best Local Similarity 100.0%; Pred. No. 0.0018;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
      ||||||||||
Db 1 SEVKMDAEFR 10

RESULT 6
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C;Species: Ursus maritimus (polar bear)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: B60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: B60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match 100.0%; Score 49; DB 2; Length 57;
  Best Local Similarity 100.0%; Pred. No. 0.0018;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
      ||||||||||
Db 1 SEVKMDAEFR 10

RESULT 7
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor protein gene.
A;Reference number: PQ0438; MUID:93075180; PMID:1445331
A;Accession: PQ0438
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83657
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

  Query Match 100.0%; Score 49; DB 2; Length 82;
  Best Local Similarity 100.0%; Pred. No. 0.0027;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
      ||||||||||
Db 12 SEVKMDAEFR 21

RESULT 8
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing

  Query Match 100.0%; Score 49; DB 1; Length 695;
  Best Local Similarity 100.0%; Pred. No. 0.028;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
      ||||||||||
Db 592 SEVKMDAEFR 601

RESULT 9
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibitor; proteinase nexin II (PN-II)

N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular form; amyloid protein precursor splice form APP(695); amyloid protein precursor splice form APP(751); amyloid protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44017; B44017; A03134; A29030; A47584; A47585; S02638; S00707; S00925; A38949; A30320; B30320; C30320; A31087; A24668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S32539; S48148; S48692; S51186; S51185; S51184; S51183; A54238; I58075; I52250; S09010; S10737; S24127; S43644
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Beyreuther, K.; Mueller-Hill, B.
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-protein precursor gene.
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor.
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein diagnostic assays.
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486

A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen, S.G.; Bots, G.T.; Luyendijk, W.; Frangione, B.
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrhage, Dutch type.
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer's disease.
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson, L.; O'dahl, S.; Nemens, E.; White, J.A.; Sadovnick, A.D.; Ball, M.J.; Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, G.M.; Bird, T.D.; Schellenberg, G.D.
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region.
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA

A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B.
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides.
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease.
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Keuren, M.L.; Patterson, D.; Pagan, S.; Kurnit, D.M.; Neve, R.L.
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K.
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor of Alzheimer's disease.

A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B.
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N.
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three patients with sporadic Alzheimer's disease.
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>

R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain: coding and noncoding regions of the fetal precursor mRNA are expressed in the cortex.
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603 as Val, GTG for residue 604 as Glu, GAG for residue 605 as Leu, CTT for residue 607 as Pro, CCC for residue 608 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 655 as Ser
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.

  Query Match   100.0%; Score 49; DB 1; Length 770;
  Best Local Similarity   100.0%; Pred. No. 0.032;
  Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SEVKMDAEFR 10
              ||||||||||
Db   667 SEVKMDAEFR 676

RESULT 10
S23094
beta-amyloid protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase.
A;Reference number: S23094; MUID:92316198; PMID:1618299
A;Accession: S23094
A;Molecule type: protein
A;Residues: 1-33 <KOJ>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

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Qy   1 SEVKMDAEF 9
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Db   1 SEVKMDAEF 9

RESULT 11
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse

N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>
A;Cross-references: EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid; transmembrane protein

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Db   592 SEVKMDAEF 600

RESULT 12
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251

R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core protein.
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain.
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of both Alzheimer's disease and Down's syndrome.
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

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Db 592 SEVKMDAEF 600

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JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773

R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein:
developmental regulation of its gene expression.
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
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proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid
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Db   644 SEVKMDSEYR 653

RESULT 14
E89026
protein F13A2.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: E89026
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for
investigating biology.
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and
www_sanger.ac.uk/Projects/C_elegans/ for a list of authors
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103,
1999; and Science 285, 1493, 1999
A;Accession: E89026
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-142 <STO>
A;Cross-references: GB:chr_V; PIDN:AAB69895.1; PID:g2384795; GSPDB:GN00023;
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Db   56 EIKQDAEFR 64

RESULT 15
AG1565
autolysin (amidase) homolog lin1064 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG1565
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Brandt, P.; Chakraborty, T.; Charbit, A.; Chetouani, F.; Couve, E.; de Daruvar, A.; Dehoux, P.; Domann, E.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Garcia-Del Portillo, F.; Garrido, P.; Gautier, L.; Goebel, W.; Gomez-Lopez, N.; Hain, T.; Hauf, J.; Jackson, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mata Vicente, J.; Ng, E.; Nordsiek, G.; Novella, S.; de Pablos, B.; Perez-Diaz, J.C.; Remmel, B.; Rose, M.; Rusniok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, J.; Cossart, P.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1565
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-774 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96295.1; PID:g16413523; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1064

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Title: US-09-869-414A-64
Perfect score: 49
Sequence: 1 SEVKMDAEFR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 762491

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	49	100.0	10	9	US-09-794-743-64	Sequence 64, Appl
4	49	100.0	10	9	US-09-794-748-64	Sequence 64, Appl
5	49	100.0	10	9	US-09-796-264-4	Sequence 4, Appli
6	49	100.0	10	9	US-09-794-925-64	Sequence 64, Appl
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9	49	100.0	10	10	US-09-795-903A-4	Sequence 4, Appli
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12	49	100.0	10	12	US-10-427-208-53	Sequence 53, Appl
13	49	100.0	10	15	US-10-032-818-7	Sequence 7, Appli
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32	49	100.0	67	12	US-10-437-706-1	Sequence 1, Appli
33	49	100.0	82	11	US-09-848-616-173	Sequence 173, App
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39	49	100.0	695	9	US-09-795-847-10	Sequence 10, Appl
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41	49	100.0	695	9	US-09-794-743-10	Sequence 10, Appl
42	49	100.0	695	9	US-09-794-743-14	Sequence 14, Appl
43	49	100.0	695	9	US-09-794-748-10	Sequence 10, Appl
44	49	100.0	695	9	US-09-794-748-14	Sequence 14, Appl
45	49	100.0	695	9	US-09-794-925-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-794-927-64
; Sequence 64, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-64

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; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-64

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Qy   1 SEVKMDAEFR 10
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Db   1 SEVKMDAEFR 10

RESULT 3
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; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
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; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
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US-09-794-743-64

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; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
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; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
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;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
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; GENERAL INFORMATION:
;  APPLICANT: Tang, Jordan J.N.
;  APPLICANT:  Lin, Xinli
;  APPLICANT:  Koelsch, Gerald
;  TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
;  TITLE OF INVENTION:  of Use Thereof
;  FILE REFERENCE: OMRF 179
;  CURRENT APPLICATION NUMBER: US/09/796,264
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: 09/604,608
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: 60/168,060
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: 60/177,836
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 60/178,368
;  PRIOR FILING DATE: 2000-01-27
;  PRIOR APPLICATION NUMBER: 60/210,292
;  PRIOR FILING DATE: 2000-06-08
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-796-264-4

  Query Match             100.0%;  Score 49;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10


RESULT 6
US-09-794-925-64
; Sequence 64, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
```

; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-64

Query Match 100.0%; Score 49; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
||||||||||
Db 1 SEVKMDAEFR 10

RESULT 7
US-09-681-442-64
; Sequence 64, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23

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;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-681-442-64

  Query Match             100.0%;  Score 49;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
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Db          1 SEVKMDAEFR 10


RESULT 8
US-09-845-226-4
; Sequence 4, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Jordan J.N.
;  APPLICANT:  Hong, Lin
;  APPLICANT:  Ghosh, Arun K.
;  TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
;  FILE REFERENCE: OMRF 182
;  CURRENT APPLICATION NUMBER: US/09/845,226
;  CURRENT FILING DATE:  2001-04-30
;  PRIOR APPLICATION NUMBER: 09/603,713
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: 60/168,060
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: 60/177,836
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 60/178,368
;  PRIOR FILING DATE: 2000-01-27
;  PRIOR APPLICATION NUMBER: 60/210,292
;  PRIOR FILING DATE: 2000-06-08
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-845-226-4
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Query Match 100.0%; Score 49; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SEVKMDAEFR 10
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Db          1 SEVKMDAEFR 10
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RESULT 9
US-09-795-903A-4
; Sequence 4, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-795-903A-4

Query Match 100.0%; Score 49; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SEVKMDAEFR 10
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Db          1 SEVKMDAEFR 10
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RESULT 10
US-09-869-414-64
; Sequence 64, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-869-414-64

Query Match 100.0%; Score 49; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
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Db 1 SEVKMDAEFR 10

RESULT 11
US-09-548-366-64
; Sequence 64, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 28341/6280A
; CURRENT APPLICATION NUMBER: US/09/548,366
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-548-366-64

  Query Match   100.0%; Score 49; DB 11; Length 10;
  Best Local Similarity   100.0%; Pred. No. 0.0017;
  Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SEVKMDAEFR 10
              ||||||||||
Db   1 SEVKMDAEFR 10

RESULT 12
US-10-427-208-53
; Sequence 53, Application US/10427208
; Publication No. US20030200555A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Hazuda, Daria J
; APPLICANT: Chen Dodson, Elizabeth
; APPLICANT: Lai, Ming-Tain
; APPLICANT: Xu, Min
; APPLICANT: Shi, Xiao-Ping
; APPLICANT: Simon, Adam J.
; APPLICANT: Wu, Guoxin
; APPLICANT: Li, Yueming
; APPLICANT: Register, Robert B.
; TITLE OF INVENTION: ASSAYS USING AMYLOID PRECURSOR PROTEINS WITH MODIFIED
; TITLE OF INVENTION: BETA-SECRETASE CLEAVAGE SITES TO MONITOR BETA-SECRETASE
ACTIVITY
; FILE REFERENCE: 21052
; CURRENT APPLICATION NUMBER: US/10/427,208
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-427-208-53

  Query Match   100.0%; Score 49; DB 12; Length 10;
  Best Local Similarity   100.0%; Pred. No. 0.0017;
  Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SEVKMDAEFR 10
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Db   1 SEVKMDAEFR 10

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RESULT 13
US-10-032-818-7
; Sequence 7, Application US/10032818
; Publication No. US20030092629A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Jordan J.N.
;  APPLICANT:  Koelsch, Gerald
;  APPLICANT:  Ghosh, Arun K.
;  TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
;  FILE REFERENCE: 2932.1006-007
;  CURRENT APPLICATION NUMBER: US/10/032,818
;  CURRENT FILING DATE:  2001-12-28
;  PRIOR APPLICATION NUMBER: US 60/275,756
;  PRIOR FILING DATE: 2001-03-14
;  PRIOR APPLICATION NUMBER: US 60/258,705
;  PRIOR FILING DATE: 2000-12-28
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-10-032-818-7

  Query Match             100.0%;  Score 49;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10


RESULT 14
US-10-354-955-1
; Sequence 1, Application US/10354955
; Publication No. US20030171291A1
; GENERAL INFORMATION:
;  APPLICANT: Gary Christie
;  APPLICANT:  Ishrut Hussain
;  APPLICANT:  David J. Powell
;  TITLE OF INVENTION: No. US20030171291A1el Treatment
;  FILE REFERENCE: P32448
;  CURRENT APPLICATION NUMBER: US/10/354,955
;  CURRENT FILING DATE:  2003-01-30
;  PRIOR APPLICATION NUMBER: 09/693,744
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 9925136.5
;  PRIOR FILING DATE: 1999-10-22
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 11
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; TYPE: PRT
; ORGANISM: human
US-10-354-955-1

  Query Match   100.0%; Score 49; DB 12; Length 11;
  Best Local Similarity   100.0%; Pred. No. 0.0019;
  Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SEVKMDAEFR 10
              ||||||||||
Db   2 SEVKMDAEFR 11

RESULT 15
US-10-354-955-3
; Sequence 3, Application US/10354955
; Publication No. US20030171291A1
; GENERAL INFORMATION:
; APPLICANT: Gary Christie
; APPLICANT: Ishrut Hussain
; APPLICANT: David J. Powell
; TITLE OF INVENTION: No. US20030171291A1el Treatment
; FILE REFERENCE: P32448
; CURRENT APPLICATION NUMBER: US/10/354,955
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 09/693,744
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 9925136.5
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein with maltose binding protein attached at
residue 1'
US-10-354-955-3

  Query Match   100.0%; Score 49; DB 12; Length 11;
  Best Local Similarity   100.0%; Pred. No. 0.0019;
  Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SEVKMDAEFR 10
              ||||||||||
Db   2 SEVKMDAEFR 11

Search completed: January 21, 2004, 09:41:42
Job time : 3.00765 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:16:19 ; Search time 2.06501 Seconds
(without alignments)
1249.644 Million cell updates/sec

Title: US-09-869-414A-64
Perfect score: 49
Sequence: 1 SEVKMDAEFR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	49	100.0	35	4	Q8WZ99	Q8wz99 homo sapien
2	49	100.0	82	4	Q16020	Q16020 homo sapien
3	49	100.0	82	4	Q16014	Q16014 homo sapien
4	49	100.0	82	4	Q16019	Q16019 homo sapien
5	49	100.0	113	13	Q8JH58	Q8jh58 chelydra se
6	49	100.0	534	13	O93296	O93296 gallus gall
7	49	100.0	569	13	Q9PVL1	Q9pvl1 gallus gall
8	49	100.0	695	11	Q60496	Q60496 cavia sp. p
9	49	100.0	695	13	Q9DGJ8	Q9dgj8 gallus gall
10	49	100.0	751	13	Q9DGJ7	Q9dgj7 gallus gall
11	49	100.0	770	6	Q9TUI0	Q9tui0 sus scrofa
12	44	89.8	79	11	O35463	O35463 cricetulus
13	44	89.8	218	11	Q8BPV5	Q8bpv5 mus musculu
14	44	89.8	384	11	Q8BPC7	Q8bpc7 mus musculu
15	44	89.8	607	11	Q99K32	Q99k32 mus musculu
16	44	89.8	695	11	P97487	P97487 mus musculu
17	43	87.8	693	13	Q98SG0	Q98sg0 xenopus lae
18	43	87.8	695	13	Q98SF9	Q98sf9 xenopus lae
19	43	87.8	747	13	Q91963	Q91963 xenopus. ap
20	42	85.7	423	2	O52379	O52379 ralstonia s
21	42	85.7	423	2	Q45693	Q45693 burkholderi
22	39	79.6	142	5	O16896	O16896 caenorhabdi
23	36	73.5	630	2	Q93IK4	Q93ik4 vibrio sp.
24	35	71.4	317	17	Q96ZT2	Q96zt2 sulfolobus
25	35	71.4	419	2	Q8GHI9	Q8ghi9 pigmentipha
26	35	71.4	774	16	Q92CV7	Q92cv7 listeria in
27	35	71.4	2148	5	Q8IPL5	Q8ipl5 drosophila
28	34	69.4	239	10	Q9FNG2	Q9fng2 arabidopsis
29	34	69.4	254	5	Q8IK90	Q8ik90 plasmodium
30	34	69.4	605	16	Q9L1F6	Q9l1f6 streptomyce
31	34	69.4	626	16	Q8ZCN4	Q8zcn4 yersinia pe
32	34	69.4	1192	10	Q94BS1	Q94bs1 arabidopsis
33	34	69.4	1261	10	Q9LU30	Q9lu30 arabidopsis
34	34	69.4	3262	4	Q13788	Q13788 homo sapien
35	33	67.3	302	9	Q37840	Q37840 bacteriopha
36	33	67.3	438	2	Q9AIK4	Q9aik4 bilophila w
37	33	67.3	449	16	Q8D1Z2	Q8d1z2 wiggleswort
38	33	67.3	582	16	Q8KFP0	Q8kfp0 chlorobium
39	33	67.3	621	4	Q9H9Y1	Q9h9y1 homo sapien
40	33	67.3	711	16	Q8EFW4	Q8efw4 shewanella
41	33	67.3	1027	4	Q9BWX2	Q9bwx2 homo sapien
42	33	67.3	1245	10	Q9C7F8	Q9c7f8 arabidopsis
43	32	65.3	143	4	Q9H935	Q9h935 homo sapien
44	32	65.3	161	16	Q98FZ2	Q98fz2 rhizobium l
45	32	65.3	286	2	Q8VNV1	Q8vnv1 chlorobium

ALIGNMENTS

RESULT 1
Q8WZ99
ID Q8WZ99 PRELIMINARY; PRT; 35 AA.
AC Q8WZ99;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

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DE   Amyloid protein (Fragment).
GN   APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wakutani Y., Ninomiya H., Iwata H., Tanaka S., Urakami K., Adachi Y.,
RA   Wada-Isoe K., Yamagata K., Ohono K., Tsubuki S., Saido T.,
RA   Hashimoto T., Iwatsubo T., Nakashima K.;
RT   "Novel missense mutation (D678N) of amyloid precursor protein gene in
RT   a Japanese pedigree of familial Alzheimer's disease.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB066441; BAB71958.1; -.
FT   NON_TER       1      1
FT   NON_TER      35     35
SQ   SEQUENCE   35 AA;  4084 MW;  49D7D17289743B71 CRC64;

  Query Match             100.0%;  Score 49;  DB 4;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 0.0045;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db         12 SEVKMDAEFR 21


RESULT 2
Q16020
ID   Q16020      PRELIMINARY;      PRT;    82 AA.
AC   Q16020;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61383; AAB26265.2; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8882 MW;  F534AA5AE5D9230A CRC64;

  Query Match             100.0%;  Score 49;  DB 4;  Length 82;
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  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
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Db         13 SEVKMDAEFR 22


RESULT 3
Q16014
ID   Q16014      PRELIMINARY;      PRT;    82 AA.
AC   Q16014;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S60721; AAB26263.2; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8972 MW;  F534AA5B3EA9230A CRC64;

  Query Match             100.0%;  Score 49;  DB 4;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db         13 SEVKMDAEFR 22


RESULT 4
Q16019
ID   Q16019      PRELIMINARY;      PRT;    82 AA.
AC   Q16019;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
```

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RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61380; AAB26264.2; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8938 MW;  F534AA50E579230A CRC64;

  Query Match             100.0%;  Score 49;  DB 4;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db         13 SEVKMDAEFR 22


RESULT 5
Q8JH58
ID   Q8JH58      PRELIMINARY;      PRT;   113 AA.
AC   Q8JH58;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Amyloid beta protein (Fragment).
OS   Chelydra serpentina serpentina (common snapping turtle).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX   NCBI_TaxID=134619;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21876906; PubMed=11882478;
RA   Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT   "Octylphenol (OP) alters the expression of members of the amyloid
RT   protein family in the hypothalamus of the snapping turtle, Chelydra
RT   serpentina serpentina.";
RL   Environ. Health Perspect. 110:269-275(2002).
DR   EMBL; AF541917; AAN04908.1; -.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   113 AA;  12750 MW;  72515C930496E053 CRC64;

  Query Match             100.0%;  Score 49;  DB 13;  Length 113;
  Best Local Similarity   100.0%;  Pred. No. 0.015;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy          1 SEVKMDAEFR 10
              ||||||||||
Db         10 SEVKMDAEFR 19


RESULT 6
O93296
ID   O93296      PRELIMINARY;      PRT;   534 AA.
AC   O93296;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Amyloid protein (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98337885; PubMed=9671674;
RA   Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA   Milligan C.E.;
RT   "Increased production of amyloid precursor protein provides a
RT   substrate for caspase-3 in dying motoneurons.";
RL   J. Neurosci. 18:5869-5880(1998).
DR   EMBL; AF042098; AAC25052.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   534 AA;  60597 MW;  FB53ECC2E66D4C92 CRC64;

  Query Match             100.0%;  Score 49;  DB 13;  Length 534;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db        431 SEVKMDAEFR 440


RESULT 7
Q9PVL1
ID   Q9PVL1      PRELIMINARY;      PRT;   569 AA.
AC   Q9PVL1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APP.
OS   Gallus gallus (Chicken).
```

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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT   "What the evolution of the amyloid protein precursor supergene family
RT   tells us about its function.";
RL   Neurochem. Int. 0:0-0(2000).
DR   EMBL; AF030341; AAF12698.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   569 AA;  64753 MW;  0AB8BB851863A19D CRC64;

  Query Match             100.0%;  Score 49;  DB 13;  Length 569;
  Best Local Similarity   100.0%;  Pred. No. 0.08;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db        467 SEVKMDAEFR 476


RESULT 8
Q60496
ID   Q60496      PRELIMINARY;      PRT;   695 AA.
AC   Q60496;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Putative amyloid precursor protein.
OS   Cavia sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10143;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
DR   EMBL; X97631; CAA66230.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
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DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78701 MW;  5196A0C4017F16AB CRC64;

  Query Match             100.0%;  Score 49;  DB 11;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 0.099;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db        592 SEVKMDAEFR 601


RESULT 9
Q9DGJ8
ID   Q9DGJ8      PRELIMINARY;      PRT;   695 AA.
AC   Q9DGJ8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein 695 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289218; AAG00593.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78565 MW;  F201ED02AEC86D95 CRC64;

  Query Match             100.0%;  Score 49;  DB 13;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 0.099;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db        592 SEVKMDAEFR 601


RESULT 10
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Q9DGJ7
ID   Q9DGJ7      PRELIMINARY;      PRT;   751 AA.
AC   Q9DGJ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein 751 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289219; AAG00594.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   751 AA;  84705 MW;  E78E9413A8033D84 CRC64;

  Query Match             100.0%;  Score 49;  DB 13;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db        648 SEVKMDAEFR 657


RESULT 11
Q9TUI0
ID   Q9TUI0      PRELIMINARY;      PRT;   770 AA.
AC   Q9TUI0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Amyloid precursor protein.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid Precursor Protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB032550; BAA84580.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   770 AA;  86961 MW;  5F7A1DCB2BCC583E CRC64;

  Query Match             100.0%;  Score 49;  DB 6;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db        667 SEVKMDAEFR 676


RESULT 12
O35463
ID   O35463      PRELIMINARY;      PRT;    79 AA.
AC   O35463;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Alzheimer's amyloid beta protein (Fragment).
GN   BETA APP.
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sambamurti K., Pinnix I., Gandhi S.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF030413; AAB86608.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001255; Beta-APP.
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DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      79     79
SQ   SEQUENCE   79 AA;  8538 MW;  37F2C6C3BFF3F597 CRC64;

  Query Match             89.8%;  Score 44;  DB 11;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEF 9
              |||||||||
Db         16 SEVKMDAEF 24


RESULT 13
Q8BPV5
ID   Q8BPV5      PRELIMINARY;      PRT;   218 AA.
AC   Q8BPV5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Amyloid beta (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK052448; BAC34997.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   218 AA;  24118 MW;  95B55AFDAE1D0EF5 CRC64;

  Query Match             89.8%;  Score 44;  DB 11;  Length 218;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEF 9
              |||||||||
Db        115 SEVKMDAEF 123


RESULT 14
Q8BPC7
ID   Q8BPC7      PRELIMINARY;      PRT;   384 AA.
AC   Q8BPC7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Amyloid beta (Fragment).
OS   Mus musculus (Mouse).
```

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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK076506; BAC36369.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   384 AA;  43990 MW;  A81B1AD8AE683173 CRC64;

  Query Match             89.8%;  Score 44;  DB 11;  Length 384;
  Best Local Similarity   100.0%;  Pred. No. 0.61;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEF 9
              |||||||||
Db        281 SEVKMDAEF 289


RESULT 15
Q99K32
ID   Q99K32      PRELIMINARY;      PRT;   607 AA.
AC   Q99K32;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical 68.4 kDa protein (Fragment).
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005490; AAH05490.1; -.
DR   HSSP; P05067; 1AAP.
DR   MGD; MGI:88059; App.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
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DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
FT   NON_TER   1   1
SQ   SEQUENCE   607 AA; 68391 MW; BF802214CBA7D172 CRC64;

  Query Match   89.8%; Score 44; DB 11; Length 607;
  Best Local Similarity   100.0%; Pred. No. 0.98;
  Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 SEVKMDAEF 9
              |||||||||
Db        504 SEVKMDAEF 512
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Search completed: January 21, 2004, 09:25:08
Job time : 3.06501 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:15:44 ; Search time 0.497132 Seconds
(without alignments)
945.960 Million cell updates/sec

Title: US-09-869-414A-64
Perfect score: 49
Sequence: 1 SEVKMDAEFR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	100.0	57	1	A4_URSMA	Q29149 ursus marit
2	49	100.0	58	1	A4_CANFA	Q28280 canis famil
3	49	100.0	58	1	A4_RABIT	Q28748 oryctolagus
4	49	100.0	58	1	A4_SHEEP	Q28757 ovis aries
5	49	100.0	59	1	A4_BOVIN	Q28053 bos taurus
6	49	100.0	751	1	A4_SAISC	Q95241 s amyloid b
7	49	100.0	770	1	A4_CAVPO	Q60495 c amyloid b
8	49	100.0	770	1	A4_HUMAN	P05067 h amyloid b
9	49	100.0	770	1	A4_MACFA	P53601 m amyloid b
10	49	100.0	770	1	A4_PIG	P79307 s amyloid b
11	44	89.8	770	1	A4_MOUSE	P12023 m amyloid b
12	44	89.8	770	1	A4_RAT	P08592 r amyloid b
13	37	75.5	269	1	T2S1_STRFI	O52512 streptomyce
14	34	69.4	3562	1	PGCV_CHICK	Q90953 gallus gall
15	34	69.4	4563	1	APB_HUMAN	P04114 homo sapien
16	33	67.3	927	1	CC15_SCHPO	Q09822 schizosacch
17	32	65.3	263	1	Y683_HALN1	Q9hri2 halobacteri

18	32	65.3	354	1	BCPA_CHLLT	Q46135 chlorobium
19	32	65.3	365	1	BCPA_CHLTE	Q46393 chlorobium
20	32	65.3	776	1	OSTA_VIBVU	Q8ded5 vibrio vuln
21	32	65.3	1906	1	YFA0_ANASP	Q8ym40 anabaena sp
22	31	63.3	81	1	RS16_CLOPE	Q8xjp4 clostridium
23	31	63.3	178	1	YJGA_HAEIN	P45076 haemophilus
24	31	63.3	183	1	YJGA_ECOLI	P26650 escherichia
25	31	63.3	198	1	TNF4_MOUSE	P43488 mus musculu
26	31	63.3	279	1	RFA2_SCHPO	Q92373 schizosacch
27	31	63.3	346	1	PA6A_HUMAN	Q9npb6 homo sapien
28	31	63.3	346	1	PA6A_MOUSE	Q9z101 mus musculu
29	31	63.3	416	1	TRPB_RHILO	Q98cn7 rhizobium l
30	31	63.3	479	1	Y098_MYCPN	P75535 mycoplasma
31	31	63.3	1024	1	Y075_MYCGE	P47321 mycoplasma
32	30	61.2	78	1	RL31_RICCN	Q92jd0 rickettsia
33	30	61.2	78	1	RL31_RICPR	Q9ze47 rickettsia
34	30	61.2	197	1	OM26_HAEIN	Q57483 haemophilus
35	30	61.2	351	1	HI82_RHIME	Q92121 rhizobium m
36	30	61.2	356	1	RF1_BACSU	P45872 bacillus su
37	30	61.2	394	1	EFTU_BUCAI	O31297 buchnera ap
38	30	61.2	400	1	YF74_ARCFU	O28698 archaeoglob
39	30	61.2	419	1	P47K_PSECL	P31521 pseudomonas
40	30	61.2	463	1	YDI4_SCHPO	Q92342 schizosacch
41	30	61.2	464	1	SPN5_SCHPO	P48010 schizosacch
42	30	61.2	595	1	SYK_MOUSE	Q99mn1 mus musculu
43	30	61.2	656	1	V091_FOWPV	O72896 fowlpox vir
44	30	61.2	666	1	ZP2_RABIT	P48829 oryctolagus
45	30	61.2	681	1	THIC_YERPE	Q8zaq2 yersinia pe

ALIGNMENTS

```
RESULT 1
A4_URSMA
ID   A4_URSMA       STANDARD;      PRT;    57 AA.
AC   Q29149;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Ursus maritimus (Polar bear) (Thalarctos maritimus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX   NCBI_TaxID=29073;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
```

```
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56128; CAA39593.1; -.
DR   PIR; B60045; B60045.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   NON_TER      57     57
SQ   SEQUENCE   57 AA;  6172 MW;  84209D88EBA82DFA CRC64;

  Query Match             100.0%;  Score 49;  DB 1;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.0019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10


RESULT 2
A4_CANFA
ID   A4_CANFA       STANDARD;      PRT;    58 AA.
AC   Q28280;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
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RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X56125; CAA39590.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6285 MW;  8469D488A2E12DFA CRC64;

  Query Match             100.0%;  Score 49;  DB 1;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.0019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          2 SEVKMDAEFR 11


RESULT 3
A4_RABIT
ID   A4_RABIT       STANDARD;      PRT;    58 AA.
AC   Q28748;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X56129; CAA39594.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             100.0%;  Score 49;  DB 1;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.0019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10


RESULT 4
A4_SHEEP
ID   A4_SHEEP       STANDARD;      PRT;    58 AA.
AC   Q28757;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
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OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X56130; CAA39595.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             100.0%;  Score 49;  DB 1;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.0019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db          1 SEVKMDAEFR 10


RESULT 5
A4_BOVIN
ID   A4_BOVIN       STANDARD;      PRT;    59 AA.
AC   Q28053;
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DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X56124; CAA39589.1; -.
DR   EMBL; X56126; CAA39591.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   DOMAIN       59    >59       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      59     59
SQ   SEQUENCE   59 AA;  6414 MW;  F43469D488A2E12D CRC64;

  Query Match             100.0%;  Score 49;  DB 1;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 0.0019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
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```
Db          2 SEVKMDAEFR 11

RESULT 6
A4_SAISC
ID   A4_SAISC       STANDARD;      PRT;   751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE   APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE   CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amorim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
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CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC       nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=Q95241-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q95241-2; Sequence=Not described;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clatherin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-linked glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
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CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Amyloid; Alternative splicing.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    751       A4 PROTEIN.
FT   CHAIN        18    668       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    652       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       653    751       C99 (POTENTIAL).
FT   CHAIN       653    694       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       653    692       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       669    751       C83 (POTENTIAL).
FT   CHAIN       669    694       P3(42) (POTENTIAL).
FT   CHAIN       669    692       P3(40) (POTENTIAL).
FT   CHAIN       693    751       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       695    751       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       702    751       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       721    751       C31 (POTENTIAL).
FT   DOMAIN       18    680       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    681    704       POTENTIAL.
FT   DOMAIN      705    751       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
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FT   DOMAIN       181     188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN       291     341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN       316     344       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       363     428       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       504     521       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN       713     732       INTERACTION WITH G(O)-ALPHA
FT                                  (BY SIMILARITY).
FT   DOMAIN       230     260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN       274     280       POLY-THR.
FT   SITE         144     144       REQUIRED FOR COPPER(II) REDUCTION
FT                                  (BY SIMILARITY).
FT   ACT_SITE     301     302       REACTIVE BOND.
FT   SITE         652     653       CLEAVAGE (BY BETA-SECRETASE)
FT                                  (BY SIMILARITY).
FT   SITE         653     654       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE         668     669       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                  (BY SIMILARITY).
FT   SITE         685     685       INVOLVED IN FREE RADICAL PROPAGATION
FT                                  (BY SIMILARITY).
FT   SITE         687     687       INVOLVED IN OXIDATIVE REACTIONS
FT                                  (BY SIMILARITY).
FT   SITE         692     693       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                  (BY SIMILARITY).
FT   SITE         694     695       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                  (BY SIMILARITY).
FT   SITE         701     702       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                  (BY SIMILARITY).
FT   SITE         705     715       BASOLATERAL SORTING SIGNAL
FT                                  (BY SIMILARITY).
FT   SITE         720     721       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                                  (BY SIMILARITY).
FT   SITE         738     741       ENDOCYTOSIS SIGNAL.
FT   SITE         740     743       NPXY MOTIF.
FT   METAL        137     137       COPPER (BY SIMILARITY).

  Query Match             100.0%;  Score 49;  DB 1;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 0.024;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db        648 SEVKMDAEFR 657


RESULT 7
A4_CAVPO
ID   A4_CAVPO       STANDARD;      PRT;   770 AA.
AC   Q60495; Q60496;
DT   15-SEP-2003 (Rel. 42, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE   protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE   P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE   CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
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GN   APP.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Liver;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
RN   [2]
RP   INTERACTION OF BETA-APP40 WITH APOE.
RX   MEDLINE=98007700; PubMed=9349544;
RA   Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA   Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT   "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT   cerebral capillary sequestration and blood-brain barrier transport of
RT   circulating Alzheimer's amyloid beta.";
RL   J. Neurochem. 69:1995-2004(1997).
RN   [3]
RP   PROCESSING.
RX   MEDLINE=20084499; PubMed=10619481;
RA   Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA   Bigl V.;
RT   "Guinea-pig primary cell cultures provide a model to study expression
RT   and amyloidogenic processing of endogenous amyloid precursor
RT   protein.";
RL   Neuroscience 95:243-254(2000).
RN   [4]
RP   GAMMA-SECRETASE PROCESSING.
RX   MEDLINE=20576391; PubMed=11035007;
RA   Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA   Ziani-Cherif C., Onstead L., Sambamurti K.;
RT   "A novel gamma -secretase assay based on detection of the putative
RT   C-terminal fragment-gamma of amyloid beta protein precursor.";
RL   J. Biol. Chem. 276:481-487(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC   physiological functions on the surface of neurons relevant to
CC   neurite growth, neuronal adhesion and axonogenesis. Involved in
CC   cell mobility and transcription regulation through protein-protein
CC   interactions (By similarity). Can promote transcription activation
CC   through binding to APBB1/Tip60 and inhibit Notch signaling through
CC   interaction with Numb (By similarity). Couples to apoptosis-
CC   inducing pathways such as those mediated by G(O) and JIP (By
CC   similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC   Acts as a kinesin I membrane receptor, mediating the axonal
CC   transport of beta-secretase and presenilin 1 (By similarity). May
CC   be involved in copper homeostasis/oxidative stress through copper
CC   ion reduction (By similarity). In vitro, copper-metallated APP
CC   induces neuronal death directly or is potentiated through Cu(II)-
CC   mediated low-density lipoprotein oxidation (By similarity). Can
CC   regulate neurite outgrowth through binding to components of the
CC   extracellular matrix such as heparin and collagen I and IV (By
CC   similarity). The splice isoforms that contain the BPTI domain

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CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC       and apoliproteins E and J in the CSF and to HDL particles in
CC       plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).
CC       Associates with microtubules in the presence of ATP and in a
CC       kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC       all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC       ApoE3 appears to be the preferred amyloid binding isoform, while
CC       the apoE4 isoform-beta-APP40 complex is capable of being
CC       transported across the blood-brain barrier.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated pits
CC       (By similarity). During maturation, the immature APP (N-
CC       glycosylated in the endoplasmic reticulum) moves to the Golgi
CC       complex where complete maturation occurs (O-glycosylated and
CC       sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC       APP is released into the extracellular space and the C-terminal is
CC       internalized to endosomes and lysosomes (By similarity). Some APP
CC       accumulates in secretory transport vesicles leaving the late Golgi
CC       compartment and returns to the cell surface (By similarity). APP
CC       sorts to the basolateral surface in epithelial cells (By
CC       similatity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms, missing exons 7,8 and 15, seem to
CC         exist. The L-isoforms, missing exon 15, are referred to as
CC         appicans;
CC       Name=APP770;
CC         IsoId=Q60495-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC   -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC       brain. The longer isoforms containing the BPTI domain are
CC       predominantly expressed in peripheral organs such as muscle and
CC       liver.
CC   -!- INDUCTION: Increased levels during neuronal differentiation.
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
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CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue (By similarity). The NPXY site is also involved in
CC       clatherin-mediated endocytosis.
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC       gamma-secretase yields P3 peptides. This is the major secretory
CC       pathway and is nonamyloidogenic. Alternatively,
CC       presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC       beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC       and amyloid-beta 42 (Abeta42), major components of amyloid
CC       plaques, and the corresponding cytotoxic C-terminal fragments
CC       (CTFs).
CC   -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC       apoptosis (By similarity).
CC   -!- PTM: N- and O-linked glycosylated. O-linkage of chondroitin
CC       sulfate to the L-APP isoforms produces the APP proteoglycan core
CC       proteins, the appicans (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific (By similarity).
CC       Phosphorylation can affect APP processing, neuronal
CC       differentiation and interaction with other proteins.
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X97631; CAA66230.1; -.
DR   EMBL; X99198; CAA67589.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
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DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (BY SIMILARITY).
FT   CHAIN        18    671       SOLUBLE APP-BETA (BY SIMILARITY).
FT   CHAIN       672    770       CTF-ALPHA (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       CTF-BETA (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59) (BY SIMILARITY).
FT   CHAIN       714    770       GAMMA-CTF(57) (BY SIMILARITY).
FT   CHAIN       740    770       C31 (BY SIMILARITY).

  Query Match             100.0%;  Score 49;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db        667 SEVKMDAEFR 676


RESULT 8
A4_HUMAN
ID   A4_HUMAN       STANDARD;      PRT;   770 AA.
AC   P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q9BT38;
AC   Q9UCB6; Q9UQ58;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE   nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE   alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE   (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE   P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE   (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE   secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE   (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE   (Amyloid intracellular domain 50) (AID(50)); C31].
GN   APP OR A4 OR AD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=87144572; PubMed=2881207;
RA   Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA   Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
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RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [5]
RP ERRATUM, AND REVISIONS.
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL Gene 102:291-292(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC TISSUE=Leukocyte;
RX MEDLINE=92268136; PubMed=1587857;
RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RL J. Biol. Chem. 267:10804-10809(1992).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [10]
RP ERRATUM, AND REVISIONS.
RA Mita S., Sadlock J., Herbert J., Schon E.A.;
RL Nucleic Acids Res. 16:11402-11402(1988).
RN [11]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [12]
RP SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [13]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";
RL Science 245:651-653(1989).
RN [14]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the

RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [15]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [16]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [17]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [18]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Beher D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [19]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [20]
RP SEQUENCE OF 672-681.
RC TISSUE=Brain cortex;
RX MEDLINE=88035004; PubMed=3312495;
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tourtellotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RT microvessels.";
RL J. Neurochem. 49:1394-1401(1987).
RN [21]
RP SEQUENCE OF 674-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffiotti U., Gajdusek D.C.;

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RT   "Characterization and chromosomal localization of a cDNA encoding
RT   brain amyloid of Alzheimer's disease.";

  Query Match             100.0%;  Score 49;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db        667 SEVKMDAEFR 676


RESULT 9
A4_MACFA
ID   A4_MACFA       STANDARD;      PRT;   770 AA.
AC   P53601; Q95KN7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC   TISSUE=Cerebellum;
RX   MEDLINE=91273117; PubMed=1905108;
RA   Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT   "Homology of the amyloid beta protein precursor in monkey and human
RT   supports a primate model for beta amyloidosis in Alzheimer's
RT   disease.";
RL   Am. J. Pathol. 138:1423-1435(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
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CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC       nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=P53601-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clatherin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
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CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-linked glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M58727; AAA36829.1; -.
DR   EMBL; M58726; AAA36828.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (POTENTIAL).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       688    770       C83 (POTENTIAL).
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FT   CHAIN        688    713       P3(42) (POTENTIAL).
FT   CHAIN        688    711       P3(40) (POTENTIAL).
FT   CHAIN        712    770       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN        714    770       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN        721    770       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN        740    770       C31 (POTENTIAL).
FT   DOMAIN        18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     700    723       POTENTIAL.
FT   DOMAIN       724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN       291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN       391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN       732    751       INTERACTION WITH G(O)-ALPHA
FT                                  (BY SIMILARITY).
FT   DOMAIN       230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN       274    280       POLY-THR.
FT   SITE         144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                  (BY SIMILARITY).
FT   ACT_SITE     301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE         671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                  (BY SIMILARITY).
FT   SITE         672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE         687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                  (BY SIMILARITY).
FT   SITE         704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                  (BY SIMILARITY).
FT   SITE         706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                  (BY SIMILARITY).
FT   SITE         711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                  (BY SIMILARITY).
FT   SITE         713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                  (BY SIMILARITY).
FT   SITE         720    721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                  (BY SIMILARITY).
FT   SITE         724    734       BASOLATERAL SORTING SIGNAL
FT                                  (BY SIMILARITY).
FT   SITE         739    740       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                                  (BY SIMILARITY).
FT   SITE         757    760       ENDOCYTOSIS SIGNAL.
FT   SITE         759    762       NPXY MOTIF.

  Query Match             100.0%;  Score 49;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db        667 SEVKMDAEFR 676


RESULT 10
A4_PIG
ID   A4_PIG         STANDARD;      PRT;   770 AA.
AC   P79307; Q29023; Q9TUI0;
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DT   01-NOV-1997 (Rel. 35, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid precursor protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-136 FROM N.A.
RC   TISSUE=Small intestine;
RA   Winteroe A.K., Fredholm M.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 667-723 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
```

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CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC       nuclei of neurons (By similarity).
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clatherin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-linked glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
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CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB032550; BAA84580.1; -.
DR   EMBL; Z84022; CAB06313.1; -.
DR   EMBL; X56127; CAA39592.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       C83 (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59).
FT   CHAIN       714    770       GAMMA-CTF(57).
FT   CHAIN       721    770       GAMMA-CTF(50) (BY SIMILARITY).
FT   CHAIN       740    770       C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT   DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700    723       POTENTIAL.
FT   DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
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FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      135    155       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732    751       INTERACTION WITH G(O)-ALPHA (BY
FT                                 SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                 (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                 (BY SIMILARITY).
FT   SITE        672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                 (BY SIMILARITY).
FT   SITE        704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                 (BY SIMILARITY).
FT   SITE        706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                 (BY SIMILARITY).
FT   SITE        711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                 (BY SIMILARITY).
FT   SITE        713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                 (BY SIMILARITY).

  Query Match             100.0%;  Score 49;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              ||||||||||
Db        667 SEVKMDAEFR 676


RESULT 11
A4_MOUSE
ID   A4_MOUSE       STANDARD;      PRT;   770 AA.
AC   P12023; P97487; P97942; Q99K32;
DT   01-OCT-1989 (Rel. 12, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE   Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE   (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE   40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE   C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE   (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE   (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE   (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE   50) (AID(50)); C31].
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88106489; PubMed=3322280;
RA   Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT   "Complementary DNA for the mouse homolog of the human amyloid beta
RT   protein precursor.";
RL   Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN   [2]
RP   REVISIONS.
RA   Yamada T.;
RL   Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=92096458; PubMed=1756177;
RA   de Strooper B., van Leuven F., van den Berghe H.;
RT   "The amyloid beta protein precursor or proteinase nexin II from mouse
RT   is closer related to its human homolog than previously reported.";
RL   Biochim. Biophys. Acta 1129:141-143(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=SAMP8; TISSUE=Hippocampus;
RX   PubMed=11235921;
RA   Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
RA   Alvarez J., Morley J.E.;
RT   "Molecular cloning, expression, and regulation of hippocampal amyloid
RT   precursor protein of senescence accelerated mouse (SAMP8).";
RL   Biochem. Cell Biol. 79:57-67(2001).
RN   [5]
RP   SEQUENCE OF 1-19 FROM N.A.
RX   MEDLINE=92209998; PubMed=1555768;
RA   Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA   Sakai Y.;
RT   "Positive and negative regulatory elements for the expression of the
RT   Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL   Gene 112:189-195(1992).
RN   [6]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
RN [8]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domesticus.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [9]
RP SEQUENCE OF 656-737 FROM N.A.
RC STRAIN=129/Sv;
RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA Loring J.F., Goate A.M.;
RT "Introduction of six mutations into the mouse genome using 'Hit and
RT Run' gene-targeting: introduction of familial Alzheimer's disease
RT mutations into the mouse amyloid precursor protein gene and
RT humanization of the A-beta fragment.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN [10]
RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
RX PubMed=8510506;
RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
RT "Regional distribution of the alternatively spliced isoforms of beta
RT APP RNA transcript in the brain of normal, heterozygous and
RT homozygous weaver mutant mice as revealed by in situ hybridization
RT histochemistry.";
RL Brain Res. Mol. Brain Res. 17:340-346(1993).
RN [11]
RP INTERACTION WITH KNS2.
RX PubMed=11144355;
RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
RT "Axonal transport of amyloid precursor protein is mediated by direct
RT binding to the kinesin light chain subunit of kinesin-I.";
RL Neuron 28:449-459(2000).
RN [12]
RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
RP THR-743; TYR-757; ASN-759 AND TYR-762.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1

RT   scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL   J. Neurosci. 21:6597-6607(2001).
RN   [13]
RP   INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
RX   MEDLINE=22028091; PubMed=11912189;
RA   Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
RT   "Interaction of Alzheimer's beta-amyloid precursor family proteins
RT   with scaffold proteins of the JNK signaling cascade.";
RL   J. Biol. Chem. 277:20070-20078(2002).
RN   [14]
RP   INTERACTION OF CTF PEPTIDES WITH NUMB.
RX   PubMed=12011466;
RA   Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
RA   Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
RT   "The gamma-secretase-generated intracellular domain of beta-amyloid
RT   precursor protein binds Numb and inhibits Notch signaling.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
RN   [15]
RP   GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
RX   PubMed=11553691;
RA   Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
RT   "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
RT   gamma-secretase is rapidly degraded but distributes partially in a
RT   nuclear fraction of neurones in culture.";
RL   J. Neurochem. 78:1168-1178(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC   physiological functions on the surface of neurons relevant to
CC   neurite growth, neuronal adhesion and axonogenesis. Involved in
CC   cell mobility and transcription regulation through protein-protein
CC   interactions. Can promote transcription activation through binding
CC   to APBB1/Tip60 and inhibit Notch signaling through interaction
CC   with Numb. Couples to apoptosis-inducing pathways such as those
CC   mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
CC   similarity). Acts as a kinesin I membrane receptor, mediating the
CC   axonal transport of beta-secretase and presenilin 1. May be
CC   involved in copper homeostasis/oxidative stress through copper ion
CC   reduction. Can regulate neurite outgrowth through binding to
CC   components of the extracellular matrix such as heparin and
CC   collagen I and IV (By similarity). The splice isoforms that
CC   contain the BPTI domain possess protease inhibitor activity (By
CC   similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC   with metal-reducing activity. Bind transient metals such as
CC   copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC   only weakly transient metals and have little reducing activity due
CC   to substitutions of transient metal chelating residues. Beta-APP42
CC   may activate mononuclear phagocytes in the brain and elicit
CC   inflammatory responses. Promotes both tau aggregation and TPK II-
CC   mediated phosphorylation (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC   peptides, including C31, are potent enhancers of neuronal
CC   apoptosis.
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC   cytoplasmic proteins, including APBB family members, the APBA
CC   family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
CC   its serine phosphorylation. Also interacts with GPCR-like protein
CC   BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via

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CC       BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
CC       MT-binding domains (By similarity). Associates with microtubules
CC       in the presence of ATP and in a kinesin-dependent manner (By
CC       similarity). Interacts, through a C-terminal domain, with GNAO1
CC       (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
CC       neurons (By similarity). Beta-amyloid associates with HADH2 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
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  Query Match             89.8%;  Score 44;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEF 9
              |||||||||
Db        667 SEVKMDAEF 675
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RESULT 12
A4_RAT
ID   A4_RAT          STANDARD;      PRT;   770 AA.
AC   P08592;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
DE   APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE   amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE   C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE   fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
DE   Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
GN   APP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88312583; PubMed=2900758;
RA   Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA   Seeburg P.H.;
RT   "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT   in rat brain suggests a role in cell contact.";
RL   EMBO J. 7:1365-1370(1988).
RN   [2]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89183625; PubMed=2648331;
RA   Kang J., Mueller-Hill B.;
RT   "The sequence of the two extra exons in rat preA4.";
RL   Nucleic Acids Res. 17:2130-2130(1989).
RN   [3]
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RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX PubMed=11483588;
RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT family resembling gamma-secretase-like cleavage of Notch.";
RL J. Biol. Chem. 276:35235-35238(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX PubMed=8624099;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "APP gene family. Alternative splicing generates functionally related
RT isoforms.";
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN [5]
RP TISSUE SPECIFICITY OF APPICAN.
RX PubMed=7744833;
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
RA Mytilineou C., Margolis R.U., Robakis N.K.;
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT brain and is produced by astrocytes but not by neurons in primary
RT neural cultures.";
RL J. Biol. Chem. 270:11839-11844(1995).
RN [6]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX PubMed=8996834;
RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT "Expression of the APP gene family in brain cells, brain development
RT and aging.";
RL Gerontology 43:119-131(1997).
RN [7]
RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP TYR-762.
RX PubMed=9930726;
RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RA Suzuki T., Nairn A.C., Greengard P.;
RT "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
RT Alzheimer's amyloid precursor protein.";
RL J. Neurochem. 72:549-556(1999).
RN [8]
RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF HIS-732 AND HIS-733.
RX PubMed=10024358;
RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,
RA Valenza C., Prochiantz A., Allinquant B.;
RT "The amyloid precursor protein interacts with Go heterotrimeric
RT protein within a cell compartment specialized in signal
RT transduction.";
RL J. Neurosci. 19:1717-1727(1999).
RN [9]
RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX MEDLINE=95256193; PubMed=7737970;
RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT "The chondroitin sulfate attachment site of appican is formed by
RT splicing out exon 15 of the amyloid precursor gene.";
RL J. Biol. Chem. 270:10388-10391(1995).
RN [10]
RP BETA-AMYLOID METAL-BINDING.
RX PubMed=10386999;

RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA Bush A.I.;
RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT peroxide through metal ion reduction.";
RL Biochemistry 38:7609-7616(1999).
RN [11]
RP BETA-AMYLOID ZINC BINDING.
RX MEDLINE=99343552; PubMed=10413512;
RA Liu S.T., Howlett G., Barrow C.J.;
RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
RT of the A beta peptide of Alzheimer's disease.";
RL Biochemistry 38:9373-9378(1999).
RN [12]
RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
RP GLY-704.
RX PubMed=11959460;
RA Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
RT peptide 1-42-associated oxidative stress and neurotoxicity.";
RL Biochim. Biophys. Acta 1586:190-198(2001).
RN [13]
RP PHOSPHORYLATION.
RX PubMed=9085254;
RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
RA Greengard P., Suzuki T.;
RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
RT cultured cells.";
RL Mol. Med. 3:111-123(1997).
RN [14]
RP PHOSPHORYLATION ON SER-730.
RX PubMed=10329382;
RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
RA Greengard P., Nairn A.C., Suzuki T.;
RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
RT precursor protein at Ser655 by a novel protein kinase.";
RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
RN [15]
RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
RP THR-743.
RX MEDLINE=99274744; PubMed=10341243;
RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
RA Kirino Y., Greengard P., Suzuki T.;
RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
RT during neuronal differentiation.";
RL J. Neurosci. 19:4421-4427(1999).
RN [16]
RP PHOSPHORYLATION ON THR-743.
RX PubMed=10936190;
RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
RT protein by cyclin-dependent kinase 5.";
RL J. Neurochem. 75:1085-1091(2000).
RN [17]
RP CARBOHYDRATE STRUCTURE OF APPICAN.

RX PubMed=11479316;
RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
RA Sugahara K., Robakis N.K.;
RT "Appican, the proteoglycan form of the amyloid precursor protein,
RT contains chondroitin sulfate E in the repeating disaccharide region
RT and 4-O-sulfated galactose in the linkage region.";
RL J. Biol. Chem. 276:37155-37160(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP. Inhibits
CC G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
CC mediating the axonal transport of beta-secretase and presenilin 1
CC (By similarity). May be involved in copper homeostasis/oxidative
CC stress through copper ion reduction. Can regulate neurite
CC outgrowth through binding to components of the extracellular
CC matrix such as heparin and collagen I and IV (By similarity). The
CC splice isoforms that contain the BPTI domain possess protease
CC inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC only weakly transient metals and have little reducing activity due
CC to substitutions of transient metal chelating residues. Beta-APP42
CC may activate mononuclear phagocytes in the brain and elicit
CC inflammatory responses. Promotes both tau aggregation and TPK II-
CC mediated phosphorylation (By similarity).
CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC extracellular matrix and may regulate neurite outgrowth in the
CC brain.
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity). Interacts,
CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
CC associates with HADH2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clatherin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the

Query Match 89.8%; Score 44; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SEVKMDAEF 9
              |||||||||
Db        667 SEVKMDAEF 675


RESULT 13
T2S1_STRFI
ID   T2S1_STRFI     STANDARD;      PRT;   269 AA.
AC   O52512;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Type II restriction enzyme SfiI (EC 3.1.21.4) (Endonuclease SfiI)
DE   (R.SfiI).
GN   SFIIR.
OS   Streptomyces fimbriatus.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=68197;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   van Cott E.M., Moran L.S., Slatko B.E., Wilson G.G.;
RT   "Characterization of the SfiI restriction and modification genes.";
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Recognizes the double-stranded sequence GGCCNNNNNGGCC
CC       and cleaves before N-9.
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC       specific double-stranded fragments with terminal 5'-phosphates.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF039750; AAB95365.1; -.
DR   REBASE; 1655; SfiI.
KW   Restriction system; Hydrolase; Nuclease; Endonuclease.
SQ   SEQUENCE   269 AA;  31044 MW;  3C48499BAA5205EA CRC64;

  Query Match             75.5%;  Score 37;  DB 1;  Length 269;
  Best Local Similarity   70.0%;  Pred. No. 2.6;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEFR 10
              |:: ||||||
Db        115 SQLPMDAEFR 124


RESULT 14
PGCV_CHICK
ID   PGCV_CHICK     STANDARD;      PRT;  3562 AA.
AC   Q90953; Q90945;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
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DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Versican core protein precursor (Large fibroblast proteoglycan)
DE   (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
GN   CPSG2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS V0 AND V1).
RC   STRAIN=White leghorn; TISSUE=Limb bud;
RX   MEDLINE=93300846; PubMed=8314802;
RA   Shinomura T., Nishida Y., Ito K., Kimata K.;
RT   "cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan
RT   expressed during chondrogenesis in chick limb buds. Alternative
RT   spliced multiforms of PG-M and their relationships to versican.";
RL   J. Biol. Chem. 268:14461-14469(1993).
CC   -!- FUNCTION: May play a role in intercellular signaling and in
CC       connecting cells with the extracellular matrix. May take part in
CC       the regulation of cell motility, growth and differentiation. Binds
CC       hyaluronic acid.
CC   -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=V0;
CC         IsoId=Q90953-1; Sequence=Displayed;
CC       Name=V1;
CC         IsoId=Q90953-2; Sequence=VSP_003093;
CC   -!- TISSUE SPECIFICITY: Prechondrogenic condensation area of
CC       developing limb buds.
CC   -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development
CC       (By similarity).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 2 link domains.
CC   -!- SIMILARITY: Contains 2 EGF-like domains.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC   -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X60226; CAA42787.1; -.
DR   EMBL; D13542; BAA02742.1; -.
DR   PIR; A47171; A47171.
DR   HSSP; P00740; 1EDM.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR007110; Ig-like.
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DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR000538; Link.
DR   InterPro; IPR000436; Sushi_SCR_CCP.
DR   Pfam; PF00008; EGF; 2.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00059; lectin_c; 1.
DR   Pfam; PF00084; sushi; 1.
DR   Pfam; PF00193; Xlink; 2.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 2.
DR   SMART; SM00032; CCP; 1.
DR   SMART; SM00034; CLECT; 1.
DR   SMART; SM00179; EGF_CA; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00445; LINK; 2.
DR   PROSITE; PS00010; ASX_HYDROXYL; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01187; EGF_CA; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS01241; LINK; 2.
KW   Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW   Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW   Hyaluronic acid; Alternative splicing.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27   3562       VERSICAN CORE PROTEIN.
FT   DOMAIN       27    143       IG-LIKE V-TYPE.
FT   DOMAIN      166    243       LINK 1.
FT   DOMAIN      264    345       LINK 2.
FT   DOMAIN     3254   3290       EGF-LIKE 1.
FT   DOMAIN     3292   3328       EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     3341   3455       C-TYPE LECTIN.
FT   DOMAIN     3460   3518       SUSHI.
FT   DISULFID     44    129       BY SIMILARITY.
FT   DISULFID    171    242       BY SIMILARITY.
FT   DISULFID    195    216       BY SIMILARITY.
FT   DISULFID    269    344       BY SIMILARITY.
FT   DISULFID    293    314       BY SIMILARITY.
FT   DISULFID   3258   3269       BY SIMILARITY.
FT   DISULFID   3263   3278       BY SIMILARITY.
FT   DISULFID   3280   3289       BY SIMILARITY.
FT   DISULFID   3296   3307       BY SIMILARITY.
FT   DISULFID   3301   3316       BY SIMILARITY.
FT   DISULFID   3318   3327       BY SIMILARITY.
FT   DISULFID   3334   3345       BY SIMILARITY.
FT   DISULFID   3362   3454       BY SIMILARITY.
FT   DISULFID   3430   3446       BY SIMILARITY.
FT   DISULFID   3461   3504       BY SIMILARITY.
FT   DISULFID   3490   3517       BY SIMILARITY.
FT   CARBOHYD    163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    235    235       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    329    329       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    529    529       N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT   CARBOHYD    709    709       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    948    948       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1409   1409       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1479   1479       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1523   1523       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1530   1530       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1625   1625       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1751   1751       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1988   1988       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2088   2088       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2089   2089       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2507   2507       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2642   2642       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2679   2679       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2748   2748       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2762   2762       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   3069   3069       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   3194   3194       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   3232   3232       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   3545   3545       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    485   1411       Missing (in isoform V1).
FT                                /FTId=VSP_003093.
SQ   SEQUENCE   3562 AA;  388078 MW;  9BC566E88C1602D2 CRC64;

  Query Match             69.4%;  Score 34;  DB 1;  Length 3562;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SEVKMDAEF 9
              | :|:||||
Db       1709 STIKLDAEF 1717


RESULT 15
APB_HUMAN
ID   APB_HUMAN      STANDARD;      PRT;  4563 AA.
AC   P04114; O00502; Q13787;
DT   01-NOV-1986 (Rel. 03, Created)
DT   01-NOV-1986 (Rel. 03, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
DE   B-48 (Apo B-48)].
GN   APOB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87016385; PubMed=3763409;
RA   Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
RA   Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
RT   "Complete cDNA and derived protein sequence of human apolipoprotein
RT   B-100.";
RL   Nucleic Acids Res. 14:7501-7503(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
```

RX MEDLINE=88003974; PubMed=3652907;
RA Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,
RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
RT "DNA sequence of the human apolipoprotein B gene.";
RL DNA 6:363-372(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87008488; PubMed=3759943;
RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
RA Gotto A.M. Jr., Chan L.;
RT "The complete cDNA and amino acid sequence of human apolipoprotein
RT B-100.";
RL J. Biol. Chem. 261:12918-12921(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87041416; PubMed=3464946;
RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
RA Lee N., Brewer H.B. Jr.;
RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
RT derived amino acid sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=87161758; PubMed=3030729;
RA Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
RA Zannis V.I.;
RT "The complete sequence and structural analysis of human
RT apolipoprotein B-100: relationship between apoB-100 and apoB-48
RT forms.";
RL EMBO J. 5:3495-3507(1986).
RN [6]
RP SEQUENCE OF 709-906 FROM N.A.
RX MEDLINE=85270450; PubMed=3860836;
RA Deeb S.S., Motulsky A.G., Albers J.J.;
RT "A partial cDNA clone for human apolipoprotein B.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
RN [7]
RP SEQUENCE OF 3056-3159 FROM N.A.
RX MEDLINE=86041888; PubMed=3903660;
RA Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
RA Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
RT "Human apolipoprotein B: identification of cDNA clones and
RT characterization of mRNA.";
RL Nucleic Acids Res. 13:6937-6953(1985).
RN [8]
RP SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A.
RX MEDLINE=86093680; PubMed=3841204;
RA Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
RA Bjursell G.;
RT "Molecular cloning of human apolipoprotein B cDNA.";
RL Nucleic Acids Res. 13:8813-8826(1985).
RN [9]
RP SEQUENCE OF 3109-4563 FROM N.A.
RX MEDLINE=85300528; PubMed=2994225;
RA Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F.,
RA Urdea M.S., Levy-Wilson B., Powell L.M., Pease R.J., Eddy R.,
RA Nakai H., Byers M., Priestley L.M., Robertson E., Rall L.B.,

RA Betsholtz C., Shows T.B., Mahley R.W., Scott J.;
RT "Human apolipoprotein B: structure of carboxyl-terminal domains,
RT sites of gene expression, and chromosomal localization.";
RL Science 230:37-43(1985).
RN [10]
RP SEQUENCE OF 1-291 FROM N.A.
RX MEDLINE=86149325; PubMed=3513177;
RA Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
RA Chen G.C., Kirsher S.W., McEnroe G., Kane J.P.;
RT "Isolation of a cDNA clone encoding the amino-terminal region of
RT human apolipoprotein B.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).
RN [11]
RP SEQUENCE OF 1-1670 FROM N.A.
RX MEDLINE=86287319; PubMed=3461454;
RA Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W.,
RA Yamanaka M., Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
RT "Analysis of cDNA clones encoding the entire B-26 region of human
RT apolipoprotein B.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
RN [12]
RP PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
RX MEDLINE=88018019; PubMed=3659919;
RA Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
RA Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
RA Gotto A.M. Jr., Li W.-H., Chan L.;
RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-
RT specific in-frame stop codon.";
RL Science 238:363-366(1987).
RN [13]
RP DOMAINS.
RX MEDLINE=87039351; PubMed=3773997;
RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
RA Levy-Wilson B., Scott J.;
RT "Complete protein sequence and identification of structural domains
RT of human apolipoprotein B.";
RL Nature 323:734-738(1986).
RN [14]
RP DOMAINS.
RA Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,
RA Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M.,
RA Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.;
RT "Sequence, structure, receptor-binding domains and internal repeats
RT of human apolipoprotein B-100.";
RL Nature 323:738-742(1986).
RN [15]
RP CALCIUM-BINDING DATA.
RX MEDLINE=86242245; PubMed=3087360;
RA Dashti N., Lee D.M., Mok T.;
RT "Apolipoprotein B is a calcium binding protein.";
RL Biochem. Biophys. Res. Commun. 137:493-499(1986).
RN [16]
RP PALMITOYLATION OF CYS-1112.
RX MEDLINE=20143590; PubMed=10679026;
RA Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.;

RT "Palmitoylation of apolipoprotein B is required for proper
RT intracellular sorting and transport of cholesteroyl esters and
RT triglycerides.";
RL Mol. Biol. Cell 11:721-734(2000).
RN [17]
RP VARIANT SER-4338.
RX MEDLINE=91071750; PubMed=1979313;
RA Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,
RA Cunny G., Cambien F., Roizes G.;
RT "Detection by denaturing gradient gel electrophoresis of a new
RT polymorphism in the apolipoprotein B gene.";
RL Hum. Genet. 86:91-93(1990).
RN [18]
RP VARIANT FDB GLN-3527.
RX MEDLINE=89098975; PubMed=2563166;
RA Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
RA McCarthy B.J.;
RT "Association between a specific apolipoprotein B mutation and
RT familial defective apolipoprotein B-100.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
RN [19]
RP VARIANT LEU-2739.
RX MEDLINE=91016974; PubMed=2216805;
RA Huang L.-S., Gavish D., Breslow J.L.;
RT "Sequence polymorphism in the human apoB gene at position 8344.";
RL Nucleic Acids Res. 18:5922-5922(1990).
RN [20]
RP VARIANT FDB CYS-3558.
RX MEDLINE=95190020; PubMed=7883971;
RA Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A.,
RA Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
RT "Familial ligand-defective apolipoprotein B. Identification of a new
RT mutation that decreases LDL receptor binding affinity.";
RL J. Clin. Invest. 95:1225-1234(1995).
RN [21]
RP VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
RP AND THR-4481.
RX MEDLINE=97044521; PubMed=8889592;
RA Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,
RA Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
RT "Detection of new variants in the apolipoprotein B (Apo B) gene by
RT PCR-SSCP.";
RL Hum. Mutat. 8:282-285(1996).
RN [22]
RP VARIANTS FDB GLN-3527 AND CYS-3558.
RX MEDLINE=97403938; PubMed=9259199;
RA Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
RA Krempf M., Giraudet P., Junien C., Boileau C.;
RT "Familial ligand-defective apolipoprotein B-100: simultaneous
RT detection of the ARG3500-->GLN and ARG3531-->CYS mutations in a
RT French population.";
RL Hum. Mutat. 10:160-163(1997).
RN [23]
RP VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432
RP AND ILE-3921.
RX MEDLINE=98141125; PubMed=9490296;
RA Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;

RT "Screening for mutations of the apolipoprotein B gene causing
RT hypocholesterolemia.";
RL Hum. Genet. 102:44-49(1998).
CC -!- FUNCTION: APOLIPOPROTEIN B IS A MAJOR PROTEIN CONSTITUENT OF
CC CHYLOMICRONS, VLDL AND LDL. IT FUNCTIONS AS A RECOGNITION SIGNAL
CC FOR THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY
CC THE APOB/E RECEPTOR.

Query Match 69.4%; Score 34; DB 1; Length 4563;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 EVKMDAEFR 10
              |||:| :||
Db       1483 EVKIDGQFR 1491
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Search completed: January 21, 2004, 09:23:05
Job time : 2.49713 secs